



SEQUENCE LISTING

<110> Benjanin, Stephane
Tanaka, Hiroaki

<120> HUMAN CDNAS AND PROTEINS AND USES THEREOF

<130> 91.US5.DIV

<140> US 09/992,095

<141> 2001-11-13

<150> US 09/924,340

<151> 2001-08-06

<150> PCT/IB01/01715

<151> 2001-08-06

<150> US 60/305,456

<151> 2001-07-13

<150> US 60/302,277

<151> 2001-06-29

<150> US 60/298,698

<151> 2001-06-15

<150> US 60/293,574

<151> 2001-05-25

<160> 112

<170> JPatent

<210> 1

<211> 2016

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..1434

<220>

<221> CDS

<222> 1435..1836

<220>

<221> 3'UTR

<222> 1837..2016

<220>

<221> polyA_signal

<222> 1965..1970

<220>

<221> polyA_site

<222> 2001..2016

<400> 1

#9

RECEIVED

AUG 20 2002

TECH CENTER 1600/2900

aaggtctctc	tgc	atg	cata	caccaag	gaa	aagccac	atg	aggacata	aac	caggaag	aga	60			
gccatcacca	aga	acccg	aa	catgcgg	aca	ccctgat	ctc	ggacttct	tag	ccttcaga	aac	120			
cgttgccaca	gtttt	gatga	tcatct	ctct	cccaacca	ag	atgg	tgaaa	aagcaaaaa	aac	180				
gtggtgaatc	ttggag	caat	cgcaca	aggc	atgaa	acgct	tcca	atttct	gttaa	actgc	240				
tgtgagccag	ggaca	attcc	tgatgc	ctcc	atcctag	cag	ctgc	ccttgga	tctact	atgc	300				
ggcattcttc	tgattc	attt	ttctcc	attt	gtgctg	tttt	tctctg	tgat	gtga	atccat	360				
ccctatccat	tatgtc	atgc	ctccat	cttt	tgctg	cttct	tcag	attgca	ctgag	ccata	420				
agaggaagcc	cctgtg	gttg	ccagag	cagc	cttg	ttcctg	gaat	gtgctc	gtttt	gttca	480				
ccgctgcaac	cgtggc	aaact	ggccag	agt	gatgaa	agg	caccac	gtga	acatc	accaa	540				
gaaaggactt	tcccgg	ggac	gctct	cccat	tgtggg	caac	aagcg	aaaacc	agaag	ctgca	600				
gtggaatgca	gccaag	ctct	tctacca	atg	gggag	acaag	gaaaaa	aggt	gaaga	ataaa	660				
aggaaattca	agagg	acca	gtttct	gcta	atttt	taga	gagct	gaaca	taa	acacaca	720				
taaagagggt	ccatat	attc	ctctttt	ctt	aaag	attact	tgga	ataact	gttaca	attt	780				
ccgttaataa	ttcag	ctgaa	tgtgt	ctacc	aatgt	gctta	ccaact	aaag	caatt	ggcgt	840				
ccgattgaat	gagct	gtgcc	acggg	gaaag	tgag	agccca	gcca	acctgc	tggg	tctcat	900				
ttacgatgaa	gagacca	aga	ggag	acttag	aaagg	aggat	gagg	aggaag	actttt	taga	960				
tgacattcca	ctttca	agtc	aatac	acagc	tcatt	cttga	tttaaa	agct	gattat	gggtg	1020				
caagcaactt	tcggg	ctgga	aattct	acag	aagct	ttgtct	tttcc	attct	tgatg	agagg	1080				
caaagtcccc	ggcaaca	aat	taact	cagga	gagaaa	atgg	ttttc	ctgaa	aaaa	acgata	1140				
gcttaaatat	ctacaga	aaag	accgt	aattt	ccacct	attt	tcaa	atgaaa	tcgt	gaaaaa	1200				
cacatttgga	ctagag	ctga	aaca	acttca	ctgcc	ctcaa	aacag	caaga	cagac	atccc	1260				
tcataaaaatg	aactg	acaga	atttt	tatag	ctccaa	aatct	agttc	actgc	catata	catata	1320				
gtctaaatct	gattga	atag	cagcg	tagaa	atctt	gcgaa	attact	tccc	atttct	gttt	1380				
tcgttaaaag	gtact	gtgaa	cccct	ctaaa	tgcg	gttgcc	ccttt	gcctt	gaag	atg	1437				
											Met				
											1				
gca gca tgt	cag	ctt	ctt	ctg	gag	att	acc	acc	ttc	ctg	cga	gag	acc	1485	
Ala Ala Cys	Gln	Leu	Leu	Leu	Glu	Ile	Thr	Thr	Phe	Leu	Arg	Glu	Thr		
											5	10	15		
ttt tct tgc	ctg	ccc	aga	cct	cgc	act	gag	cct	ctg	gtg	gct	tca	acg	1533	
Phe Ser Cys	Leu	Pro	Arg	Pro	Arg	Thr	Glu	Pro	Leu	Val	Ala	Ser	Thr		
											20	25	30		
gac cac acc	aaa	atg	cca	tct	caa	atg	gaa	cac	gcc	atg	gaa	acc	atg	1581	
Asp His Thr	Lys	Met	Pro	Ser	Gln	Met	Glu	His	Ala	Met	Glu	Thr	Met		
											35	40	45		
atg ttt aca	ttt	cac	aaa	ttc	gct	ggg	gat	aaa	ggc	tac	tta	aca	aag	1629	
Met Phe Thr	Phe	His	Lys	Phe	Ala	Gly	Asp	Lys	Gly	Tyr	Leu	Thr	Lys		
											50	55	60	65	
gag gac ctg	aga	gta	ctc	atg	gaa	aag	gag	ttc	cct	gga	ttt	ttg	gaa	1677	
Glu Asp Leu	Arg	Val	Leu	Met	Glu	Lys	Glu	Phe	Pro	Gly	Phe	Leu	Glu		
											70	75	80		
aat caa aaa	gac	cct	ctg	gct	gtg	gac	aaa	ata	atg	aag	gac	ctg	gac	1725	
Asn Gln Lys	Asp	Pro	Leu	Ala	Val	Asp	Lys	Ile	Met	Lys	Asp	Leu	Asp		
											85	90	95		
cag tgt aga	gat	ggc	aaa	gtg	ggc	ttc	cag	agc	ttc	ttt	tcc	cta	att	1773	
Gln Cys Arg	Asp	Gly	Lys	Val	Gly	Phe	Gln	Ser	Phe	Phe	Ser	Leu	Ile		
											100	105	110		
gcg ggc ctc	acc	att	gca	tgc	aat	gac	tat	ttt	gta	gta	cac	atg	aag	1821	
Ala Gly Leu	Thr	Ile	Ala	Cys	Asn	Asp	Tyr	Phe	Val	Val	His	Met	Lys		
											115	120	125		
cag aag gga	aag	aag	tagg	cagaaa	tgag	cagttc	gctc	ctccct	gata	agagtt				1876	
Gln Lys Gly	Lys	Lys													
											130				
gtcccaaagg	gtcgct	taag	gaat	ctgccc	cacag	cttcc	cccat	agaag	gattt	catga				1936	
gcagatcagg	acact	tagca	aatg	taaaaa	taaa	atctaa	ctct	catttg	aca	agcagag				1996	
											2016				
											2016				

<210> 2
 <211> 134
 <212> PRT

<213> Homo sapiens

<400> 2

```
Met Ala Ala Cys Gln Leu Leu Leu Glu Ile Thr Thr Phe Leu Arg Glu
1          5          10          15
Thr Phe Ser Cys Leu Pro Arg Pro Arg Thr Glu Pro Leu Val Ala Ser
          20          25          30
Thr Asp His Thr Lys Met Pro Ser Gln Met Glu His Ala Met Glu Thr
          35          40          45
Met Met Phe Thr Phe His Lys Phe Ala Gly Asp Lys Gly Tyr Leu Thr
          50          55          60
Lys Glu Asp Leu Arg Val Leu Met Glu Lys Glu Phe Pro Gly Phe Leu
65          70          75          80
Glu Asn Gln Lys Asp Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu
          85          90          95
Asp Gln Cys Arg Asp Gly Lys Val Gly Phe Gln Ser Phe Phe Ser Leu
          100          105          110
Ile Ala Gly Leu Thr Ile Ala Cys Asn Asp Tyr Phe Val Val His Met
          115          120          125
Lys Gln Lys Gly Lys Lys
130
```

<210> 3

<211> 1081

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..38

<220>

<221> CDS

<222> 39..917

<220>

<221> 3'UTR

<222> 918..1081

<220>

<221> polyA_signal

<222> 1045..1050

<220>

<221> polyA_site

<222> 1066..1081

<400> 3

```
gtccagcctg ttgctgatgc tgccgtgccc tacttgctc atg gag ctg gca ctg cgg 56
                                     Met Glu Leu Ala Leu Arg
                                     -25          -20
cgc tct ccc gtc ccg cgg tgg ttg ctg ctg ccg ctg ctg ctg ggc 104
Arg Ser Pro Val Pro Arg Trp Leu Leu Leu Leu Pro Leu Leu Leu Gly
          -15          -10          -5
ctg aac gca gga gct gtc att gac tgg ccc aca gag gag ggc aag gaa 152
Leu Asn Ala Gly Ala Val Ile Asp Trp Pro Thr Glu Glu Gly Lys Glu
          1          5          10
gta tgg gat tat gtg acg gtc cgc aag gat gcc tac atg ttc tgg tgg 200
Val Trp Asp Tyr Val Thr Val Arg Lys Asp Ala Tyr Met Phe Trp Trp
          15          20          25
```

ctc	tat	tat	gcc	acc	aac	tcc	tgc	aag	aac	ttc	tca	gaa	ctg	ccc	ctg	248
Leu	Tyr	Tyr	Ala	Thr	Asn	Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	
30					35					40					45	
gtc	atg	tgg	ctt	cag	ggc	ggg	cca	ggc	ggg	tct	agc	act	gga	ttt	gga	296
Val	Met	Trp	Leu	Gln	Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	
				50					55					60		
aac	ttt	gag	gaa	att	ggg	ccc	ctt	gac	agt	gat	ctc	aaa	cca	cgg	aaa	344
Asn	Phe	Glu	Glu	Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	
			65					70					75			
acc	acc	tgg	ctc	cag	gct	gcc	agt	ctc	cta	ttt	gtg	gat	aat	ccc	gtg	392
Thr	Thr	Trp	Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	
		80					85					90				
ggc	act	ggg	ttc	agt	tat	gtg	aat	ggg	agt	ggg	gcc	tat	gcc	aag	gac	440
Gly	Thr	Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	
	95					100					105					
ctg	gct	atg	gtg	gct	tca	gac	atg	atg	ggt	ctc	ctg	aag	acc	ttc	ttc	488
Leu	Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	
	110				115					120					125	
agt	tgc	cac	aaa	gaa	ttc	cag	aca	ggt	cca	ttc	tac	att	ttc	tca	gag	536
Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	Glu	
			130						135					140		
tcc	tat	gga	gga	aaa	atg	gca	gct	ggc	att	ggg	cta	gag	ctt	tat	aag	584
Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	Tyr	Lys	
		145						150					155			
gcc	att	cag	cga	ggg	acc	atc	aag	tgc	aac	ttt	gcg	ggg	ggt	gcc	ttg	632
Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	Val	Ala	Leu	
		160					165					170				
ggg	gat	tcc	tgg	atc	tcc	cct	ggt	gat	tcg	gtg	ctc	tcc	tgg	gga	cct	680
Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	Ser	Trp	Gly	Pro	
	175					180					185					
tac	ctg	tac	agc	atg	tct	ctt	ctc	gaa	gac	aaa	ggg	ctg	gca	gag	gtg	728
Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	Gly	Leu	Ala	Glu	Val	
	190				195					200					205	
tct	aag	ggt	gca	gag	caa	gta	ctg	aat	gcc	gta	aat	aag	ggg	ctc	tac	776
Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	Val	Asn	Lys	Gly	Leu	Tyr	
			210						215					220		
aga	gag	gcc	aca	gag	ctg	tgg	ggg	aaa	gca	gaa	atg	atc	att	gaa	cag	824
Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	Ala	Glu	Met	Ile	Ile	Glu	Gln	
		225						230					235			
gta	aaa	agg	gga	aac	act	cag	agg	cta	gcc	tgc	ttg	gct	ttt	tct	ggg	872
Val	Lys	Arg	Gly	Asn	Thr	Gln	Arg	Leu	Ala	Cys	Leu	Ala	Phe	Ser	Gly	
		240					245					250				
ggg	tac	agg	gcc	cat	ggg	tgg	tgt	tgt	caa	act	tgg	agt	cta	cac		917
Gly	Tyr	Arg	Ala	His	Gly	Trp	Cys	Cys	Gln	Thr	Trp	Ser	Leu	His		
	255					260					265					
tgaggctccc	cacatatctg	caa	aatgattg	catgctggat	aataaatctc	ttgggtctaa										977
gcagtgatgt	agtggtcct	tacagagtca	gaaagccacc	caggcctgca	agacttgctt											1037
gtccttcact	aaatgtatgg	attctattaa	aaaaaaaaaa	aaaa												1081

<210> 4

<211> 293

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..26

<400> 4

Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu Leu

-25						-20						-15					
Leu	Pro	Leu	Leu	Leu	Gly	Leu	Asn	Ala	Gly	Ala	Val	Ile	Asp	Trp	Pro		
-10						-5				1				5			
Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val	Arg	Lys	Asp		
		10						15					20				
Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	Ser	Cys	Lys	Asn		
		25					30					35					
Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	Gly	Gly	Pro	Gly	Gly		
	40					45				50							
Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	Ile	Gly	Pro	Leu	Asp	Ser		
55					60					65					70		
Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	Leu	Gln	Ala	Ala	Ser	Leu	Leu		
			75					80						85			
Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser		
		90						95					100				
Gly	Ala	Tyr	Ala	Lys	Asp	Leu	Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val		
	105					110						115					
Leu	Leu	Lys	Thr	Phe	Phe	Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro		
	120					125				130							
Phe	Tyr	Ile	Phe	Ser	Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile		
135					140					145					150		
Gly	Leu	Glu	Leu	Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn		
			155					160						165			
Phe	Ala	Gly	Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser		
		170						175						180			
Val	Leu	Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp		
	185					190						195					
Lys	Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala		
	200					205				210							
Val	Asn	Lys	Gly	Leu	Tyr	Arg	Glu	Ala	Thr	Glu	Leu	Trp	Gly	Lys	Ala		
215					220					225					230		
Glu	Met	Ile	Ile	Glu	Gln	Val	Lys	Arg	Gly	Asn	Thr	Gln	Arg	Leu	Ala		
			235					240						245			
Cys	Leu	Ala	Phe	Ser	Gly	Gly	Tyr	Arg	Ala	His	Gly	Trp	Cys	Cys	Gln		
		250						255					260				
Thr	Trp	Ser	Leu	His													
	265																

<210> 5
 <211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..83

<220>
 <221> CDS
 <222> 84..317

<220>
 <221> 3'UTR
 <222> 318..438

<220>
 <221> polyA_signal
 <222> 397..402

<220>

<221> polyA_site

<222> 423..438

<400> 5

```
atagaaaagg acatctcttg agacttcact tcagcttcac tgacttcttg actctcctct 60
tgagtaaaag gactcagcca act atg aag ttt ttt gtc ttt gct tta gtc ttg 113
                               Met Lys Phe Phe Val Phe Ala Leu Val Leu
                               -15                               -10
gct ctc atg att tcc atg att agc gct gat tca cat gaa aag aga cat 161
Ala Leu Met Ile Ser Met Ile Ser Ala Asp Ser His Glu Lys Arg His
                               -5                               1                               5
cat ggg tat aga aga aaa ttc cat gaa aag cat cat tca tac cat atc 209
His Gly Tyr Arg Arg Lys Phe His Glu Lys His His Ser Tyr His Ile
                               10                               15                               20
aca cta cta cca ctt ttt gaa gaa tca tca aag agc aat gca aat gaa 257
Thr Leu Leu Pro Leu Phe Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu
25                               30                               35                               40
aaa cac tat aat tta ctg tat act ctt tgt ttc agg ata ctt gcc ttt 305
Lys His Tyr Asn Leu Leu Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe
                               45                               50                               55
tca att gtc act tgatgatata attgcaattt aaactgttaa gctgtgttca 357
Ser Ile Val Thr
                               60
gtactgtttc tgaataatag aaatcacttc tctaaaagca ataaatttca agcacatttt 417
taaataaaaa aaaaaaaaaa a 438
```

<210> 6

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..19

<400> 6

```
Met Lys Phe Phe Val Phe Ala Leu Val Leu Ala Leu Met Ile Ser Met
                               -15                               -10                               -5
Ile Ser Ala Asp Ser His Glu Lys Arg His His Gly Tyr Arg Arg Lys
                               1                               5                               10
Phe His Glu Lys His His Ser Tyr His Ile Thr Leu Leu Pro Leu Phe
                               15                               20                               25
Glu Glu Ser Ser Lys Ser Asn Ala Asn Glu Lys His Tyr Asn Leu Leu
30                               35                               40                               45
Tyr Thr Leu Cys Phe Arg Ile Leu Ala Phe Ser Ile Val Thr
                               50                               55
```

<210> 7

<211> 968

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..31

<220>

<221> CDS

<222> 32..748

<220>

<221> 3'UTR

<222> 749..968

<220>

<221> polyA_signal

<222> 928..933

<220>

<221> polyA_site

<222> 953..968

<400> 7

```
tgatcaggac tcctcagttc accttctcac a atg agg ctc cct gct cag ctc      52
                               Met Arg Leu Pro Ala Gln Leu
                               -15
ctg ggg ctg cta atg ctc tgg gtc tct gga tcc agt ggg gat att gtg      100
Leu Gly Leu Leu Met Leu Trp Val Ser Gly Ser Ser Gly Asp Ile Val
                               -10                               1
atg act cag tct cca ctc ttc ctg ccc gtc acc cct gga gag ccg gcc      148
Met Thr Gln Ser Pro Leu Phe Leu Pro Val Thr Pro Gly Glu Pro Ala
5                               10                               15                               20
tcc atc tcc tgc agg tct agt cag agc ctc ctg cat gtt caa ggg tcc      196
Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu His Val Gln Gly Ser
                               25                               30                               35
aac tat ttg gat tgg tac cac cag aag cca ggg cag tct cca caa ctc      244
Asn Tyr Leu Asp Trp Tyr His Gln Lys Pro Gly Gln Ser Pro Gln Leu
                               40                               45                               50
ctg ata tac ttg ggt tct aat cgg gcc tcc ggg gtc cct gac agg ttc      292
Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe
                               55                               60                               65
agt ggc agt gga tca ggc aca gat ttc aca ctg aaa atc agt aga gtg      340
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
70                               75                               80
gag gct gag gat gtt ggg gtt tat tac tgc atg caa gct cta caa act      388
Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr
85                               90                               95                               100
cca ttc act ttc ggc cct ggg acc aga gtg gat atc aag cga act gtg      436
Pro Phe Thr Phe Gly Pro Gly Thr Arg Val Asp Ile Lys Arg Thr Val
                               105                               110                               115
gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa      484
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
                               120                               125                               130
tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga      532
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
135                               140                               145
gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac      580
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
150                               155                               160
tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc      628
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
165                               170                               175                               180
ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa      676
Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
                               185                               190                               195
gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca      724
Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
200                               205                               210
aag agc ttc aac agg gga gag tgt tagagggaga agtgccccc cctgctctc      778
Lys Ser Phe Asn Arg Gly Glu Cys
```


<220>

<221> 3'UTR

<222> 575..730

<400> 9

```
agatgagtgt tcagctctca gcagagaggt tagctcctct ctgcagcttg tcctgttgtc 60
tcctcaagtc tggctgagtc cggagttttt atgagcctca gaggggagga agtgcattgct 120
gattaatcca tgggcaggcc tggaaaagt ccactccag tctgcgggac ccacagcctg 180
gccctcaggc ctcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccct 240
tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
          Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
                    -10                    -5
aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
      1      5      10      15
atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
      20      25      30
ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
      35      40      45
tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
      50      55      60
ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Cys Gln Asp Asn Ser Asp Glu Glu
      65      70      75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      80      85      90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tgttatcagc 634
ctttgaaatg taggtagctt tattatccac attttgacaga tgaggaaaca gagtcagggtg 694
aagtgtcttt tccaaggcca agctcctgag ggcagg 730
```

<210> 10

<211> 107

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..14

<400> 10

```
Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
          -10          -5          1
Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
      5      10      15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
      20      25      30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
      35      40      45      50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
      55      60      65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
      70      75      80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
      85      90
```

<210> 11

<211> 733
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..253

<220>
 <221> CDS
 <222> 254..574

<220>
 <221> 3'UTR
 <222> 575..733

<400> 11
 agatgagtgt tcagctctca gcagagaggt tagctcctct ctgcagcttg tcctgttgtc 60
 tcctcaagtc tggctgagtc cggagttttt atgagcctca gaggggagga agtgcattgct 120
 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
 gccctcaggc ctcaggcctt ccttggttg aagattgggc ttcacctggg acctaccct 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
 tgagccctga gctaattaag tgctggataa gcatacctc ccagtaatcc tgttatcagc 634
 ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggtg 694
 aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

<210> 12
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..14

<400> 12
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
 -10 -5 1
 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
 5 10 15

Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 85 90

<210> 13
 <211> 732
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..253

<220>
 <221> CDS
 <222> 254..574

<220>
 <221> 3'UTR
 <222> 575..732

<400> 13
 agatgagtgt tcagctctca gcagagaggt tagctcctct ctgcagcttg tctgtttgtc 60
 tcctcaagtc tggctgagtc cggagttttt atgagcctca gaggggagga agtgcattgct 120
 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
 gccctcaggc ctcaggcctt ccttggtttg aagattgggc ttcacctggg acctaccctt 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tgc aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60
 ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
 Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
 65 70 75
 agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
 Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 80 85 90
 tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
 ctttgaaatg taggtagctt attatccaca ttttgcagat gaggaacag agtcagggtga 694
 agtgtctttt ccaaggccaa gctcctgagg gcaggggc 732

<210> 14
 <211> 107

<212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..14

<400> 14
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
 -10 -5 1
 Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
 5 10 15
 Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
 20 25 30
 Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
 35 40 45 50
 Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
 55 60 65
 Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
 70 75 80
 Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
 85 90

<210> 15
 <211> 733
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..253

<220>
 <221> CDS
 <222> 254..574

<220>
 <221> 3'UTR
 <222> 575..733

<400> 15
 agatgagtgt tcagctctca gcagagaggt tagctcctct ctgcagcttg tcctgttgtc 60
 tcctcaagtc tggctgagtc cggagttttt atgagcctca gaggggagga agtgcattgct 120
 gattaatcca tgggcaggcc tggaaaagtt cccactccag tctgcgggac ccacagcctg 180
 gccctcaggc ytcaggcctt cccaggcttg aagattgggc ttcacctggg acctaccctt 240
 tctgcctagg agc atg tct gcc tcc tgc tgc ctt tca tgg tgc cca gcc 289
 Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala
 -10 -5
 aag gct aag tcg aaa tgt ggc cca acc ttc ttc ccc tgt gcc agc ggc 337
 Lys Ala Lys Ser Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly
 1 5 10 15
 atc cat tgc atc att ggt cgc ttc cgg tgc aat ggg ttt gag gac tgt 385
 Ile His Cys Ile Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys
 20 25 30
 ccc gat ggc agc gat gaa gag aac tgc aca gca aac cct ctg ctt tgc 433
 Pro Asp Gly Ser Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys
 35 40 45
 tcc acc gcc cgc tac cac tgc aag aac ggc ctc tgt att gac aag agc 481
 Ser Thr Ala Arg Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser
 50 55 60

```

ttc atc tgc gat gga cag aat aac tgt caa gac aac agt gat gag gaa 529
Phe Ile Cys Asp Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu
  65          70          75
agc tgt gaa agt tct caa gct att ttt cca caa att act gtg tcc 574
Ser Cys Glu Ser Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
  80          85          90
tgagccctga gctaattaag tgctggataa gcatcacctc ccagtaatcc tggtatcagc 634
ctttgaaatg taggtagctt tattatccac attttgcaga tgaggaaaca gagtcagggtg 694
aagtgtcttt tccaaggcca agctcctgag ggcaggggc 733

```

```

<210> 16
<211> 107
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..14

```

```

<400> 16
Met Ser Ala Ser Cys Cys Leu Ser Trp Cys Pro Ala Lys Ala Lys Ser
          -10          -5          1
Lys Cys Gly Pro Thr Phe Phe Pro Cys Ala Ser Gly Ile His Cys Ile
  5          10          15
Ile Gly Arg Phe Arg Cys Asn Gly Phe Glu Asp Cys Pro Asp Gly Ser
  20          25          30
Asp Glu Glu Asn Cys Thr Ala Asn Pro Leu Leu Cys Ser Thr Ala Arg
  35          40          45          50
Tyr His Cys Lys Asn Gly Leu Cys Ile Asp Lys Ser Phe Ile Cys Asp
          55          60          65
Gly Gln Asn Asn Cys Gln Asp Asn Ser Asp Glu Glu Ser Cys Glu Ser
          70          75          80
Ser Gln Ala Ile Phe Pro Gln Ile Thr Val Ser
  85          90

```

```

<210> 17
<211> 1175
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..326

```

```

<220>
<221> CDS
<222> 327..1013

```

```

<220>
<221> 3'UTR
<222> 1014..1175

```

```

<220>
<221> polyA_signal
<222> 1131..1136

```

```

<220>
<221> polyA_site
<222> 1160..1175

```

<400> 17

gaagcggagc ggtctagggg gccgcgggccc cgggtcacccc ggccgggtagc agttgctgag 60
 tgtcagctag acagcagcga ctagggctcg ggcgcgggccc agatgccttt gttcaccgcc 120
 aaccccttcg agcaagacgt ggtgatgcca attgggtggaa aggagaaaat cacagaggaa 180
 taggactttt cccatccaat tttgtaacaa ctaattttaaa catagagact gaggcagcgg 240
 ctgtggacaa attgaatgta attgatgatg atgtggagga aattaagaaa tcagagcctg 300
 agcctgttta tatagatgag gataag atg gat aga gcc ctg cag gta ctt cag 353
 Met Asp Arg Ala Leu Gln Val Leu Gln

1 5

agt ata gat cca aca gat tca aaa cca gac tcc caa gac ctt ttg gat 401
 Ser Ile Asp Pro Thr Asp Ser Lys Pro Asp Ser Gln Asp Leu Leu Asp
 10 15 20 25
 tta gaa gat atc tgc caa cag atg ggt cca atg ata gat gaa aaa ctt 449
 Leu Glu Asp Ile Cys Gln Gln Met Gly Pro Met Ile Asp Glu Lys Leu
 30 35 40
 gaa gaa att gat agg aag cat tca gaa ttg tct gaa ttg aat gtt aaa 497
 Glu Glu Ile Asp Arg Lys His Ser Glu Leu Ser Glu Leu Asn Val Lys
 45 50 55
 gtc ctg gaa gct ctg gaa cta tat aac aaa ttg gtg aat gaa gca cca 545
 Val Leu Glu Ala Leu Glu Leu Tyr Asn Lys Leu Val Asn Glu Ala Pro
 60 65 70
 gtg tac tca gtc tat tca aag ctc cac cct cca gca cat tac cca cct 593
 Val Tyr Ser Val Tyr Ser Lys Leu His Pro Pro Ala His Tyr Pro Pro
 75 80 85
 gca tca tct ggg gtt cca atg cag aca tat cca gtt caa tca cat ggt 641
 Ala Ser Ser Gly Val Pro Met Gln Thr Tyr Pro Val Gln Ser His Gly
 90 95 100 105
 gga aac tat atg ggt cag agc att cac caa gta act gtt gcc caa agc 689
 Gly Asn Tyr Met Gly Gln Ser Ile His Gln Val Thr Val Ala Gln Ser
 110 115 120
 tat agc cta gga ccc gat caa att ggt cca ctg aga tct ctg cct cca 737
 Tyr Ser Leu Gly Pro Asp Gln Ile Gly Pro Leu Arg Ser Leu Pro Pro
 125 130 135
 aat gtg aat tcc tca gtg aca gca cag cct gct caa act tca tat tta 785
 Asn Val Asn Ser Ser Val Thr Ala Gln Pro Ala Gln Thr Ser Tyr Leu
 140 145 150
 agc act gga caa gac act gtt tcc aat cct act tat atg aac cag aac 833
 Ser Thr Gly Gln Asp Thr Val Ser Asn Pro Thr Tyr Met Asn Gln Asn
 155 160 165
 tct aac cta cag tca gct act ggt aca act gct tac aca cag caa atg 881
 Ser Asn Leu Gln Ser Ala Thr Gly Thr Thr Ala Tyr Thr Gln Gln Met
 170 175 180 185
 ggg atg tct gtg gat atg tca tct tat cag aac act act tcc aat ttg 929
 Gly Met Ser Val Asp Met Ser Ser Tyr Gln Asn Thr Thr Ser Asn Leu
 190 195 200
 cct caa ctg gca ggc ttt ccg gtg aca gtt cca gct cat cca gtt gca 977
 Pro Gln Leu Ala Gly Phe Pro Val Thr Val Pro Ala His Pro Val Ala
 205 210 215
 cag cag cac aca aat tac cat cag cag cct ctc ctt tagaaacaaa 1023
 Gln Gln His Thr Asn Tyr His Gln Gln Pro Leu Leu
 220 225
 tcaagcattt tcttgaaagc cttcataagt gtattattca gtccttgtga taccaacctg 1083
 aaaatatata aacttttttc cctctcaact caaaaggacc atgaataaat aaagcacaaa 1143
 aacctctctt attctgaaaa aaaaaaaaaa at 1175

<210> 18
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 18
Met Asp Arg Ala Leu Gln Val Leu Gln Ser Ile Asp Pro Thr Asp Ser
1 5 10 15
Lys Pro Asp Ser Gln Asp Leu Leu Asp Leu Glu Asp Ile Cys Gln Gln
20 25 30
Met Gly Pro Met Ile Asp Glu Lys Leu Glu Glu Ile Asp Arg Lys His
35 40 45
Ser Glu Leu Ser Glu Leu Asn Val Lys Val Leu Glu Ala Leu Glu Leu
50 55 60
Tyr Asn Lys Leu Val Asn Glu Ala Pro Val Tyr Ser Val Tyr Ser Lys
65 70 75 80
Leu His Pro Pro Ala His Tyr Pro Pro Ala Ser Ser Gly Val Pro Met
85 90 95
Gln Thr Tyr Pro Val Gln Ser His Gly Gly Asn Tyr Met Gly Gln Ser
100 105 110
Ile His Gln Val Thr Val Ala Gln Ser Tyr Ser Leu Gly Pro Asp Gln
115 120 125
Ile Gly Pro Leu Arg Ser Leu Pro Pro Asn Val Asn Ser Ser Val Thr
130 135 140
Ala Gln Pro Ala Gln Thr Ser Tyr Leu Ser Thr Gly Gln Asp Thr Val
145 150 155 160
Ser Asn Pro Thr Tyr Met Asn Gln Asn Ser Asn Leu Gln Ser Ala Thr
165 170 175
Gly Thr Thr Ala Tyr Thr Gln Gln Met Gly Met Ser Val Asp Met Ser
180 185 190
Ser Tyr Gln Asn Thr Thr Ser Asn Leu Pro Gln Leu Ala Gly Phe Pro
195 200 205
Val Thr Val Pro Ala His Pro Val Ala Gln Gln His Thr Asn Tyr His
210 215 220
Gln Gln Pro Leu Leu
225

<210> 19
<211> 844
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..111

<220>
<221> CDS
<222> 112..813

<220>
<221> 3'UTR
<222> 814..844

<400> 19
tttctgttg cctgtctcta aaccctcca cattcccgcg gtccttcaga ctgcccgag 60
agcgcgctct gcctgccgcc tgccctgcctg ccaactgaggg ttcccagcac c atg agg 117
Met Arg
-15
gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg gca gcc 165
Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala
-10 -5 1
cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa gaa act 213
Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu Glu Thr
5 10 15

gtg gca gag gtg act gag gta tct gtt gga gct aat cct gtc cag gtg	261
Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val Gln Val	
20 25 30	
gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag gag gtg	309
Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu Glu Val	
35 40 45 50	
gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac ggc aag gtg	357
Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys Val	
55 60 65	
tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag gac ccc	405
Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln Asp Pro	
70 75 80	
acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc agc aat	453
Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser Asn	
85 90 95	
gac aac aag acc ttc gac tct tcc tgc cac ttc ttt gcc aca aag tgc	501
Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys Cys	
100 105 110	
acc ctg gag ggc acc aag aag ggc cac aag ctc cac ctg gac tac atc	549
Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr Ile	
115 120 125 130	
ggg cct tgc aaa tac atc ccc cct tgc ctg gac tct gag ctg acc gaa	597
Gly Pro Cys Lys Tyr Ile Pro Pro Cys Leu Asp Ser Glu Leu Thr Glu	
135 140 145	
ttc ccc ctg cgc atg cgg gac tgg ctc aag aac gtc ctg gtc acc ctg	645
Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr Leu	
150 155 160	
tat gag agg gat gag gac aac aac ctt ctg act gag aag cag aag ctg	693
Tyr Glu Arg Asp Glu Asp Asn Asn Leu Leu Thr Glu Lys Gln Lys Leu	
165 170 175	
cgg gtg aag aag atc cat gag aat gag aag cgc ctg gag gca gga gac	741
Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly Asp	
180 185 190	
cac ccc gtg gag ctg ctg gcc cgg gac tgc cag gct gtt tca gcc agg	789
His Pro Val Glu Leu Leu Ala Arg Asp Cys Gln Ala Val Ser Ala Arg	
195 200 205 210	
aag gcc aaa atc aag agt gag atg tagaaagttg taaaatagaa aaagtggagt	843
Lys Ala Lys Ile Lys Ser Glu Met	
215	
t	844

<210> 20
 <211> 234
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17

<400> 20
 Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 -15 -10 -5
 Ala Ala Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu
 1 5 10 15
 Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
 20 25 30
 Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
 35 40 45
 Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly

50		55		60
Lys Val Cys Glu Leu Asp	Glu Asn Asn Thr Pro Met Cys Val Cys Gln			
65	70	75		
Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly	Glu Phe Glu Lys Val Cys			
80	85	90	95	
Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser	Cys His Phe Phe Ala Thr			
	100	105	110	
Lys Cys Thr Leu Glu Gly Thr Lys Lys Gly	His Lys Leu His Leu Asp			
	115	120	125	
Tyr Ile Gly Pro Cys Lys Tyr Ile Pro Pro	Cys Leu Asp Ser Glu Leu			
	130	135	140	
Thr Glu Phe Pro Leu Arg Met Arg Asp Trp	Leu Lys Asn Val Leu Val			
	145	150	155	
Thr Leu Tyr Glu Arg Asp Glu Asp Asn Asn	Leu Leu Thr Glu Lys Gln			
160	165	170	175	
Lys Leu Arg Val Lys Lys Ile His Glu Asn	Glu Lys Arg Leu Glu Ala			
	180	185	190	
Gly Asp His Pro Val Glu Leu Leu Ala Arg	Asp Cys Gln Ala Val Ser			
	195	200	205	
Ala Arg Lys Ala Lys Ile Lys Ser Glu Met				
210	215			

<210> 21
 <211> 1997
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..126

<220>
 <221> CDS
 <222> 127..1020

<220>
 <221> 3'UTR
 <222> 1021..1997

<400> 21
 atcctctaag cttttaaaata ttgcttcgat ggtctgaatt tttatttcca gggaaaaaga 60
 gagttttgtc ccacagtcag caggccacta gtttattaac ttccagtcac cttgattttt 120
 gctaaa atg aag act ctg cag tct aca ctt ctc ctg tta ctg ctt gtg 168
 Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Val
 -15 -10 -5
 cct ctg ata aag cca gca cca cca acc cag cag gac tca cgc att atc 216
 Pro Leu Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile
 1 5 10
 tat gat tat gga aca gat aat ttt gaa gaa tcc ata ttt agc caa gat 264
 Tyr Asp Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp
 15 20 25
 tat gag gat aaa tac ctg gat gga aaa aat att aag gaa aaa gaa act 312
 Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr
 30 35 40
 gtg ata ata ccc aat gag aaa agt ctt caa tta caa aaa gat gag gca 360
 Val Ile Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala
 45 50 55 60
 ata aca cca tta cct ccc aag aaa gaa aat gat gaa atg ccc acg tgt 408
 Ile Thr Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys
 65 70 75

ctg ctg tgt gtt tgt tta agt ggc tct gta tac tgt gaa gaa gtt gac	456
Leu Leu Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp	
80 85 90	
att gat gct gta cca ccc tta cca aag gaa tca gcc tat ctt tac gca	504
Ile Asp Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala	
95 100 105	
cga ttc aac aaa att aaa aag ctg act gcc aaa gat ttt gca gac ata	552
Arg Phe Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile	
110 115 120	
cct aac tta aga aga ctc gat ttt aca gga aat ttg ata gaa gat ata	600
Pro Asn Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile	
125 130 135 140	
gaa gat ggt act ttt tca aaa ctt tct ctg tta gaa gaa ctt tca ctt	648
Glu Asp Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu	
145 150 155	
gct gaa aat caa cta cta aaa ctt cca gtt ctt cct ccc aag ctc act	696
Ala Glu Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr	
160 165 170	
tta ttt aat gca aaa tac aac aaa atc aag agt agg gga atc aaa gca	744
Leu Phe Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala	
175 180 185	
aat gca ttc aaa aaa ctg aat aac ctc acc ttc ctc tac ttg gac cat	792
Asn Ala Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His	
190 195 200	
aat gcc ctg gaa tcc gtg cct ctt aat tta cca gaa agt cta cgt gta	840
Asn Ala Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val	
205 210 215 220	
att cat ctt cag ttc aac aac ata gct tca att aca gat gac aca ttc	888
Ile His Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe	
225 230 235	
tgc aag gct aat gac acc agt tac atc cgg gac cgc att gaa gag ata	936
Cys Lys Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile	
240 245 250	
cgc ctg gag ggc aat cca atc gtc ctg gga aag cat cca aac agt ttt	984
Arg Leu Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe	
255 260 265	
att tgc tta aaa aga tta ccg ata ggg tca tac ttt taacctctat	1030
Ile Cys Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe	
270 275 280	
tggtacaaca tataaatgaa agtacaccta cactaatagt ctgtctcaac aatgagtaaa	1090
ggaacttaag tattgggttta atattaacct tgtatctcat tttgaaggaa tttaatat	1150
taagcaagga tgttcaaaat cttacatata ataagtaaaa agtaagactg aatgtctacg	1210
ttcgaacaaa agtaatatga aaatatttaa acagcattac aaaatcctag tttatactag	1270
actaccattt aaaaatcatg tttttatata aatgcccaaa tttgagatgc attattccta	1330
ttactaatga tgtaagtacg aggataaata caagaaactt tcaactcttt gcctttcctg	1390
gcctttactg gatcccaaaa gcatttaagg tacatgttcc aaaaactttg aaaagctaaa	1450
tggtttcccat gatcgctcat tcttctttta tgattcatat gttattcctt ataaagtaag	1510
aactttgttt tcttcctatc aaggcagcta ttttattaaa tttttcactt agtctgagaa	1570
atagcagata gtctcatatt taggaaaact ttccaaataa aataaatgtt attctctgat	1630
aaagagctaa tacagaaatg ttcaagttat tttactttct ggtaatgtct tcagtaaaat	1690
attttcttta tctaaatatt aacattctaa gtctaccaaa aaaagtttta aactcaagca	1750
ggccaaaacc aatatgttta taagaaataa tgaaaagttc atccatttct gataaagttc	1810
tctatggcaa agtctttcaa atacgagata actgcaaaat attttccttt tatactacag	1870
aatgagaat ctcataata aattagttca agcataagat gaaaacagaa tattctgtgg	1930
tgccagtgc cactaccttc ccacccatac acatccatgt tcaactgtaac aaactgaata	1990
ttcaciaa	1997

<210> 22
 <211> 298
 <212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..19

<400> 22

Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Leu Val Pro Leu
-15 -10 -5
Ile Lys Pro Ala Pro Pro Thr Gln Gln Asp Ser Arg Ile Ile Tyr Asp
1 5 10
Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp Tyr Glu
15 20 25
Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile
30 35 40 45
Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala Ile Thr
50 55 60
Pro Leu Pro Pro Lys Lys Glu Asn Asp Glu Met Pro Thr Cys Leu Leu
65 70 75
Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp Ile Asp
80 85 90
Ala Val Pro Pro Leu Pro Lys Glu Ser Ala Tyr Leu Tyr Ala Arg Phe
95 100 105
Asn Lys Ile Lys Lys Leu Thr Ala Lys Asp Phe Ala Asp Ile Pro Asn
110 115 120 125
Leu Arg Arg Leu Asp Phe Thr Gly Asn Leu Ile Glu Asp Ile Glu Asp
130 135 140
Gly Thr Phe Ser Lys Leu Ser Leu Leu Glu Glu Leu Ser Leu Ala Glu
145 150 155
Asn Gln Leu Leu Lys Leu Pro Val Leu Pro Pro Lys Leu Thr Leu Phe
160 165 170
Asn Ala Lys Tyr Asn Lys Ile Lys Ser Arg Gly Ile Lys Ala Asn Ala
175 180 185
Phe Lys Lys Leu Asn Asn Leu Thr Phe Leu Tyr Leu Asp His Asn Ala
190 195 200 205
Leu Glu Ser Val Pro Leu Asn Leu Pro Glu Ser Leu Arg Val Ile His
210 215 220
Leu Gln Phe Asn Asn Ile Ala Ser Ile Thr Asp Asp Thr Phe Cys Lys
225 230 235
Ala Asn Asp Thr Ser Tyr Ile Arg Asp Arg Ile Glu Glu Ile Arg Leu
240 245 250
Glu Gly Asn Pro Ile Val Leu Gly Lys His Pro Asn Ser Phe Ile Cys
255 260 265
Leu Lys Arg Leu Pro Ile Gly Ser Tyr Phe
270 275

<210> 23

<211> 1746

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..9

<220>

<221> CDS

<222> 10..1212

<220>

<221> 3'UTR
 <222> 1213..1746

<220>
 <221> polyA_signal
 <222> 1709..1714

<220>
 <221> polyA_site
 <222> 1733..1746

<400> 23

```

gcctcacca atg gtt ccc ttc atc tat ctg caa gcc cac ttt aca ctc tgt      51
      Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys
      -15                               -10                               -5
tct ggg tgg tcc agc aca tac cgg gac ctc cgg aag ggt gtg tat gtg      99
Ser Gly Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val
      1                               5                               10
ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac ctg gta      147
Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val
      15                               20                               25                               30
agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att gct gcc      195
Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala
      35                               40                               45
atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg gaa ggc      243
Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly
      50                               55                               60
atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac tcc ccg      291
Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Pro
      65                               70                               75
gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc aac ctc      339
Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu
      80                               85                               90
ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag tct gaa      387
Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu
      95                               100                               105                               110
gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc gac cac      435
Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His
      115                               120                               125
tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg gag tgg      483
Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp
      130                               135                               140
tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag gat ctg      531
Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu
      145                               150                               155
aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg gac agt      579
Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser
      160                               165                               170
ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct gca gtc      627
Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val
      175                               180                               185                               190
aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gac ggt ttc      675
Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe
      195                               200                               205
tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc cct tgg      723
Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp
      210                               215                               220
aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt acc aac      771
Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn
      225                               230                               235

```

cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg cca gtg 819
 Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val
 240 245 250
 gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc atc tca 867
 Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser
 255 260 265 270
 cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag ggc ttc 915
 Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe
 275 280 285
 tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct gtc agc 963
 Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser
 290 295 300
 gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa ggc cct 1011
 Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro
 305 310 315
 ttt gtc acc ttg gac atg gaa gac tgt ggc tac aac att cca cag aca 1059
 Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr
 320 325 330
 gat gag tca acc ctc atg acc ata gcc tat gtc atg gct gcc atc tgc 1107
 Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys
 335 340 345 350
 gcc ctc ttc atg ctg cca ctc tgc ctc atg gtg tgt cag tgg cgc tgc 1155
 Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp Arg Cys
 355 360 365
 ctc cgc tgc ctg cgc cag cag cat gat gac ttt gct gat gac atc tcc 1203
 Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Ile Ser
 370 375 380
 ctg ctg aag tgaggaggcc catgggcaga agatagggat tcccctggac 1252
 Leu Leu Lys
 385
 cacacctccg tggttcactt tggtcacaag taggagacac agatggcacc tgtggccaga 1312
 gcacctcagg accctcccca cccaccaaat gcctctgcct tgatggagaa ggaaaaggct 1372
 ggcaagggtgg gttccagga ctgtacctgt aggagacaga aaagagaaga aagaagcact 1432
 ctgctggcgg gaatactctt ggtcacctca aatttaagtc gggaaattct gctgcttgaa 1492
 acttcagccc tgaacctttg tcaccattcc tttaaattct ccaacccaaa gtattcttct 1552
 tttcttagtt tcagaagtac tggcatcaca cgcagggttac cttggcgtgt gtcctgtgg 1612
 taccctggca gagaagagac caagcttggt tccctgctgg ccaaagtcag taggagagga 1672
 tgcacagttt gctatttgct ttagagacag ggactgtata aacaagccta acattggtgc 1732
 aaaaaaaaaa aaaa 1746

<210> 24
 <211> 401
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..17

<400> 24
 Met Val Pro Phe Ile Tyr Leu Gln Ala His Phe Thr Leu Cys Ser Gly
 -15 -10 -5
 Trp Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
 1 5 10 15
 Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile
 20 25 30
 Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr
 35 40 45
 Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu
 50 55 60

<221> polyA_site

<222> 1224..1239

<400> 25

```
agtcctaggat cctcacacca gctacttgca agggagaagg aaaaggccag taaggcctgg 60
gccaggagag tcccgacagg agtgtcaggt ttcaatctca gcaccagcca ctgagagcag 120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc 168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
      -20 -15 -10
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca 216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
      -5 1 5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca 264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
      10 15 20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat 312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
      25 30 35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag 360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
      40 45 50 55
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc 408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
      60 65 70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg 456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
      75 80 85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc 504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
      90 95 100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag 552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
      105 110 115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg 600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu
      120 125 130 135
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca 648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
      140 145 150
cgg cgg cac acc cgg agc gcc gag gac gac tcg gag cgg gac ccc ctg 696
Arg Arg His Thr Arg Ser Ala Glu Asp Ser Glu Arg Asp Pro Leu
      155 160 165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt 744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
      170 175 180
tca cag gag ctc ccg agc gcc gag gac aac agc ccg atg gcc agt gac 792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
      185 190 195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga 840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
      200 205 210 215
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggctgct 889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
      220 225
ggaagggcac cctctttaac ccatccctca gcaaacgcag ctcttcccaa ggaccaggctc 949
ccttgacggt ccgaggatgg gaaaggtgac aggggcatgt atggaatttg ctgcttctct 1009
ggggctccctt ccacaggagg tcctgtgaga accaaccttt gagggcccaag tcatgggggtt 1069
tcaccgcctt cctcactcca tatagaacac ctttcccaat aggaaacccc aacaggtaaa 1129
ctagaaattt ccccttcatg aaggtagaga gaaggggtct ctcccaacat atttctcttc 1189
cttgtgcctc tcctctttat cacttttaag catgaaaaaa aaaaaaaaaa 1239
```

<210> 26
 <211> 251
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 26
 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val
 -20 -15 -10
 Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
 -5 1 5
 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
 10 15 20
 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
 25 30 35 40
 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
 45 50 55
 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
 60 65 70
 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
 75 80 85
 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
 90 95 100
 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
 105 110 115 120
 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
 125 130 135
 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
 140 145 150
 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
 155 160 165
 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
 170 175 180
 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
 185 190 195 200
 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
 205 210 215
 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
 220 225

<210> 27
 <211> 1179
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..115

<220>
 <221> CDS
 <222> 116..961

<220>
 <221> 3'UTR
 <222> 962..1179


```

<220>
<221> polyA_signal
<222> 1145..1150

<220>
<221> polyA_site
<222> 1164..1179

<220>
<221> UNSURE
<222> 116
<223> Xaa = Asn,Thr

<220>
<221> UNSURE
<222> 233
<223> Xaa = Phe,Ser

<400> 27
acaaattccc aatgcagtta caggatcctg ggaagcagag tgtctggatg gaacctgagc 60
tgggtctctg actcacttct gacttttaggc gctcgaggac tgtgcccagg agcag atg 118
Met
1
cgg ctc aga gcc cag gtg cgc ctg ctt gag acc cgg gtc aaa cag caa 166
Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln Gln
5 10 15
cag gtc aag atc aag cag ctt ttg cag gag aat gaa gtc cag ttc ctt 214
Gln Val Lys Ile Lys Gln Leu Leu Gln Glu Asn Glu Val Gln Phe Leu
20 25 30
gat aaa gga gat gag aat act gtc gtt gat ctt gga agc aag agg cag 262
Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg Gln
35 40 45
tat gca gat tgt tca gag att ttc aat gat ggg tat aag ctc agt gga 310
Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly
50 55 60 65
ttt tac aaa atc aaa cct ctc cag agc cca gca gaa ttt tct gtt tat 358
Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr
70 75 80
tgt gac atg tcc gat gga gga gga tgg act gta att cag aga cga tct 406
Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg Ser
85 90 95
gat ggc agt gaa aac ttt aac aga gga tgg aaa gac tat gaa aat ggc 454
Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly
100 105 110
ttt gga amt ttt gtc caa aaa cat ggt gaa tat tgg ctg ggc aat aaa 502
Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn Lys
115 120 125
aat ctt cac ttc ttg acc act caa gaa gac tac act tta aaa atc gac 550
Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp
130 135 140 145
ctt gca gat ttt gaa aaa aat agc cgt tat gca caa tat aag aat ttc 598
Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn Phe
150 155 160
aaa gtt gga gat gaa aag aat ttc tac gag ttg aat att ggg gaa tat 646
Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr
165 170 175
tct gga aca gct gga gat tcc ctt gcg ggg aat ttt cat cct gag gtg 694
Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu Val
180 185 190

```

cag tgg tgg gct agt cac caa aga atg aaa ttc agc acg tgg gac aga	742
Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp Arg	
195 200 205	
gat cat gac aac tat gaa ggg aac tgc gca gaa gaa gat cag tct ggc	790
Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser Gly	
210 215 220 225	
tgg tgg ttt aac agg tgt cac tyt gca aac ctg aat ggt gta tac tac	838
Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr Tyr	
230 235 240	
agc ggc ccc tac acg gct aaa aca gac aat ggg att gtc tgg tac acc	886
Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr	
245 250 255	
tgg cat ggg tgg tgg tat tct ctg aaa tct gtg gtt atg aaa att agg	934
Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile Arg	
260 265 270	
cca aat gat ttt att cca aat gta att taattgctgc tgttgggctt	981
Pro Asn Asp Phe Ile Pro Asn Val Ile	
275 280	
tcgtttctgc aattcagctt tgtttaaagt gatttgaaaa atactcattc tgaacatata	1041
catgcgcaat catgataact gttgtgagta gtgcttttca ttcttctcac ttgcctttgt	1101
tacttaatgt gctttcagta cagcagatat gcaatattca ccaaataaat gtagactgtg	1161
tcaaaaaaaaa aaaaaaaaa	1179

<210> 28
 <211> 282
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> 116
 <223> Xaa = Asn,Thr

<220>
 <221> UNSURE
 <222> 233
 <223> Xaa = Phe,Ser

<400> 28

Met Arg Leu Arg Ala Gln Val Arg Leu Leu Glu Thr Arg Val Lys Gln	
1 5 10 15	
Gln Gln Val Lys Ile Lys Gln Leu Leu Glu Asn Glu Val Gln Phe	
20 25 30	
Leu Asp Lys Gly Asp Glu Asn Thr Val Val Asp Leu Gly Ser Lys Arg	
35 40 45	
Gln Tyr Ala Asp Cys Ser Glu Ile Phe Asn Asp Gly Tyr Lys Leu Ser	
50 55 60	
Gly Phe Tyr Lys Ile Lys Pro Leu Gln Ser Pro Ala Glu Phe Ser Val	
65 70 75 80	
Tyr Cys Asp Met Ser Asp Gly Gly Gly Trp Thr Val Ile Gln Arg Arg	
85 90 95	
Ser Asp Gly Ser Glu Asn Phe Asn Arg Gly Trp Lys Asp Tyr Glu Asn	
100 105 110	
Gly Phe Gly Xaa Phe Val Gln Lys His Gly Glu Tyr Trp Leu Gly Asn	
115 120 125	
Lys Asn Leu His Phe Leu Thr Thr Gln Glu Asp Tyr Thr Leu Lys Ile	
130 135 140	
Asp Leu Ala Asp Phe Glu Lys Asn Ser Arg Tyr Ala Gln Tyr Lys Asn	
145 150 155 160	
Phe Lys Val Gly Asp Glu Lys Asn Phe Tyr Glu Leu Asn Ile Gly Glu	

Tyr Ser Gly Thr Ala Gly Asp Ser Leu Ala Gly Asn Phe His Pro Glu
 165 170 175
 Val Gln Trp Trp Ala Ser His Gln Arg Met Lys Phe Ser Thr Trp Asp
 180 185 190
 Arg Asp His Asp Asn Tyr Glu Gly Asn Cys Ala Glu Glu Asp Gln Ser
 195 200 205
 Gly Trp Trp Phe Asn Arg Cys His Xaa Ala Asn Leu Asn Gly Val Tyr
 210 215 220
 Tyr Ser Gly Pro Tyr Thr Ala Lys Thr Asp Asn Gly Ile Val Trp Tyr
 225 230 235 240
 Thr Trp His Gly Trp Trp Tyr Ser Leu Lys Ser Val Val Met Lys Ile
 245 250 255
 Arg Pro Asn Asp Phe Ile Pro Asn Val Ile
 260 265 270
 275 280

<210> 29
 <211> 1118
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..344

<220>
 <221> CDS
 <222> 345..1118

<220>
 <221> polyA_site
 <222> 1103..1118

<220>
 <221> UNSURE
 <222> 30
 <223> Xaa = Glu, *

<400> 29
 aatcctagtc ttcgtttggt ccggttgacac tcttcctata gccagaggg cgagagggcc 60
 tgtggcctgg gggaaggagg acgaggttct gcctggatcc cagcaggacg ctgtgccatt 120
 tgggaacaaa ggaatagctt gcctggaatc cctgcagatc ttggggcccg aggccagtcc 180
 aacccttgga gcaggaagaa acgcaaagtt gtcaagaacc aagtcgagct gcctcagagc 240
 cgccccgcag tagctgcaga ctccgcccgc gacgtgtgcg cgcttctctg ggccagagcg 300
 agcctgtttt gtgctcgggt taagagattt gtcccagcta tacc atg ggc cgc act 356
 Met Gly Arg Thr
 cgg gaa gct ggc tgc gtg gcc gct ggt gtg gtt atc ggg gct ggt gcc 404
 Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile Gly Ala Gly Ala
 -15 -10 -5 1
 tgc tac tgt gta tac aga ctg gct tgg gga aga gac gag aac gag aaa 452
 Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp Glu Asn Glu Lys
 5 10 15
 atc tgg gac gaa gac gag gag tct acg gac acc tca kag att ggg gtt 500
 Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser Xaa Ile Gly Val
 20 25 30
 gag act gtg aaa gga gct aaa act aac gct ggg gca ggg tct ggg gcc 548
 Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala Gly Ser Gly Ala
 35 40 45
 aaa ctt cag ggt gat tca gag gtc aag cct gag gtg agt ttg gga ctc 596
 Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val Ser Leu Gly Leu

50		55		60		65	
gag gat tgt ccg ggt gta aaa gag aag gcc cat tca gga tcc cac agc	644						
Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser Gly Ser His Ser							
		70		75		80	
gga ggt ggc cta gag gcc aag gcc aag gcc ctt ttc aac acg ctg aag	692						
Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe Asn Thr Leu Lys							
		85		90		95	
gaa cag gca agt gca aag gca ggc aaa ggg gct agg gtg ggt acc atc	740						
Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg Val Gly Thr Ile							
		100		105		110	
tct ggg aac agg acc ctt gca ccg agt tta ccc tgc cca gga ggc agg	788						
Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys Pro Gly Gly Arg							
		115		120		125	
ggt gga ggc tgc cac ccc acc agg agt gga tct agg gcc ggg ggc agg	836						
Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg Ala Gly Gly Arg							
		130		135		140	
gca agt gga aaa tcc aag gga aag gcc cga agt aag agc acc agg gct	884						
Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys Ser Thr Arg Ala							
		150		155		160	
cca gct aca aca tgg cct gtc cgg aga ggc aag ttc aac ttt cct tat	932						
Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe Asn Phe Pro Tyr							
		165		170		175	
aaa att gat gat att ctg agt gct ccc gac ctc caa aag gtc ctc aac	980						
Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln Lys Val Leu Asn							
		180		185		190	
atc ctg gag cga aca aat gat cct ttt att caa gaa gta gcc ttg gtc	1028						
Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu Val Ala Leu Val							
		195		200		205	
act ctg ggt aac aat gca gca tat tca ttt aac cag aat gcc ata cgt	1076						
Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln Asn Ala Ile Arg							
		210		215		220	
gaa ttg ggt ggt gtc cca att att gca aaa aaa aaa aaa aaa	1118						
Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys Lys Lys							
		230		235			

<210> 30
 <211> 258
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<220>
 <221> UNSURE
 <222> 29
 <223> Xaa = Glu, *

<400> 30
 Met Gly Arg Thr Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile
 -20 -15 -10 -5
 Gly Ala Gly Ala Cys Tyr Cys Val Tyr Arg Leu Ala Trp Gly Arg Asp
 1 5 10
 Glu Asn Glu Lys Ile Trp Asp Glu Asp Glu Glu Ser Thr Asp Thr Ser
 15 20 25
 Xaa Ile Gly Val Glu Thr Val Lys Gly Ala Lys Thr Asn Ala Gly Ala
 30 35 40
 Gly Ser Gly Ala Lys Leu Gln Gly Asp Ser Glu Val Lys Pro Glu Val
 45 50 55 60

Ser Leu Gly Leu Glu Asp Cys Pro Gly Val Lys Glu Lys Ala His Ser
 65 70 75
 Gly Ser His Ser Gly Gly Gly Leu Glu Ala Lys Ala Lys Ala Leu Phe
 80 85 90
 Asn Thr Leu Lys Glu Gln Ala Ser Ala Lys Ala Gly Lys Gly Ala Arg
 95 100 105
 Val Gly Thr Ile Ser Gly Asn Arg Thr Leu Ala Pro Ser Leu Pro Cys
 110 115 120
 Pro Gly Gly Arg Gly Gly Gly Cys His Pro Thr Arg Ser Gly Ser Arg
 125 130 135 140
 Ala Gly Gly Arg Ala Ser Gly Lys Ser Lys Gly Lys Ala Arg Ser Lys
 145 150 155
 Ser Thr Arg Ala Pro Ala Thr Thr Trp Pro Val Arg Arg Gly Lys Phe
 160 165 170
 Asn Phe Pro Tyr Lys Ile Asp Asp Ile Leu Ser Ala Pro Asp Leu Gln
 175 180 185
 Lys Val Leu Asn Ile Leu Glu Arg Thr Asn Asp Pro Phe Ile Gln Glu
 190 195 200
 Val Ala Leu Val Thr Leu Gly Asn Asn Ala Ala Tyr Ser Phe Asn Gln
 205 210 215 220
 Asn Ala Ile Arg Glu Leu Gly Gly Val Pro Ile Ile Ala Lys Lys Lys
 225 230 235
 Lys Lys

<210> 31
 <211> 1273
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..13

<220>
 <221> CDS
 <222> 14..1048

<220>
 <221> 3'UTR
 <222> 1049..1273

<220>
 <221> polyA_signal
 <222> 1234..1239

<220>
 <221> polyA_site
 <222> 1258..1273

<400> 31
 agaggttgagg aag atg gcg tgg cga ggc tgg gcg cag aga ggc tgg ggc 49
 Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly
 -25 -20 -15
 tgc ggc cag gcg tgg ggt gcg tgc gtg ggc ggc cgc agc tgc gag gag 97
 Cys Gly Gln Ala Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu
 -10 -5 1
 ctc act gcg gtc cta acc ccg ccg cag ctc ctc gga cgc agg ttt aac 145
 Leu Thr Ala Val Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn
 5 10 15
 ttc ttt att caa caa aaa tgc gga ttc aga aaa gca ccc agg aag gtt 193

Phe	Phe	Ile	Gln	Gln	Lys	Cys	Gly	Phe	Arg	Lys	Ala	Pro	Arg	Lys	Val		
20					25					30					35		
gaa	cct	cga	aga	tca	gac	cca	ggg	aca	agt	ggg	gaa	gca	tac	aag	aga	241	
Glu	Pro	Arg	Arg	Ser	Asp	Pro	Gly	Thr	Ser	Gly	Glu	Ala	Tyr	Lys	Arg		
				40					45					50			
agt	gct	ttg	att	cct	cct	gtg	gaa	gaa	aca	gtc	ttt	tat	cct	tct	ccc	289	
Ser	Ala	Leu	Ile	Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro		
				55				60					65				
tat	cct	ata	agg	agt	ctc	ata	aaa	cct	tta	ttt	ttt	act	gtt	ggg	ttt	337	
Tyr	Pro	Ile	Arg	Ser	Leu	Ile	Lys	Pro	Leu	Phe	Phe	Thr	Val	Gly	Phe		
		70					75					80					
aca	ggc	tgt	gca	ttt	gga	tca	gct	gct	att	tgg	caa	tat	gaa	tca	ctg	385	
Thr	Gly	Cys	Ala	Phe	Gly	Ser	Ala	Ala	Ile	Trp	Gln	Tyr	Glu	Ser	Leu		
		85				90					95						
aaa	tcc	agg	gtc	cag	agt	tat	ttt	gat	ggg	ata	aaa	gct	gat	tgg	ttg	433	
Lys	Ser	Arg	Val	Gln	Ser	Tyr	Phe	Asp	Gly	Ile	Lys	Ala	Asp	Trp	Leu		
						105				110				115			
gat	agc	ata	aga	cca	caa	aaa	gaa	gga	gac	ttc	aga	aag	gag	att	aac	481	
Asp	Ser	Ile	Arg	Pro	Gln	Lys	Glu	Gly	Asp	Phe	Arg	Lys	Glu	Ile	Asn		
				120					125					130			
aag	tgg	tgg	aat	aac	cta	agt	gat	ggc	cag	cgg	act	gtg	aca	ggg	att	529	
Lys	Trp	Trp	Asn	Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile		
			135					140					145				
ata	gct	gca	aat	gtc	ctt	gta	ttc	tgt	tta	tgg	aga	gta	cct	tct	ctg	577	
Ile	Ala	Ala	Asn	Val	Leu	Val	Phe	Cys	Leu	Trp	Arg	Val	Pro	Ser	Leu		
		150					155					160					
cag	cgg	aca	atg	atc	aga	tat	ttc	aca	tcg	aat	cca	gcc	tca	aag	gtc	625	
Gln	Arg	Thr	Met	Ile	Arg	Tyr	Phe	Thr	Ser	Asn	Pro	Ala	Ser	Lys	Val		
		165				170					175						
ctt	tgt	tct	cca	atg	ttg	ctg	tca	aca	ttc	agt	cat	ttc	tcc	tta	ttt	673	
Leu	Cys	Ser	Pro	Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe		
					185					190				195			
cac	atg	gca	gca	aat	atg	tat	gtt	ttg	tgg	agc	ttc	tct	tcc	agc	ata	721	
His	Met	Ala	Ala	Asn	Met	Tyr	Val	Leu	Trp	Ser	Phe	Ser	Ser	Ser	Ile		
				200					205					210			
gtg	aac	att	ctg	ggg	caa	gag	cag	ttc	atg	gca	gtg	tac	cta	tct	gca	769	
Val	Asn	Ile	Leu	Gly	Gln	Glu	Gln	Phe	Met	Ala	Val	Tyr	Leu	Ser	Ala		
			215					220				225					
ggg	gtt	att	tcc	aat	ttt	gtc	agt	tac	gtg	ggg	aaa	gtt	gcc	aca	gga	817	
Gly	Val	Ile	Ser	Asn	Phe	Val	Ser	Tyr	Val	Gly	Lys	Val	Ala	Thr	Gly		
		230				235						240					
aga	tat	gga	cca	tca	ctt	ggg	gca	gcc	ctg	aaa	gcc	att	atc	gcc	atg	865	
Arg	Tyr	Gly	Pro	Ser	Leu	Gly	Ala	Ala	Leu	Lys	Ala	Ile	Ile	Ala	Met		
		245				250					255						
gat	aca	gca	gga	atg	atc	ctg	gga	tgg	aaa	ttt	ttt	gat	cat	gcg	gca	913	
Asp	Thr	Ala	Gly	Met	Ile	Leu	Gly	Trp	Lys	Phe	Phe	Asp	His	Ala	Ala		
		260			265				270					275			
cat	ctt	ggg	gga	gct	ctt	ttt	gga	ata	tgg	tat	gtt	act	tac	ggg	cat	961	
His	Leu	Gly	Gly	Ala	Leu	Phe	Gly	Ile	Trp	Tyr	Val	Thr	Tyr	Gly	His		
				280				285					290				
gaa	ctg	att	tgg	aag	aac	agg	gag	cgg	cta	gtg	aaa	atc	tgg	cat	gaa	1009	
Glu	Leu	Ile	Trp	Lys	Asn	Arg	Glu	Pro	Leu	Val	Lys	Ile	Trp	His	Glu		
			295					300				305					
ata	agg	act	aat	ggc	ccc	aaa	aaa	gga	ggg	ggc	tct	aag	taaaactggg			1058	
Ile	Arg	Thr	Asn	Gly	Pro	Lys	Lys	Gly	Gly	Gly	Ser	Lys					
			310				315				320						
attggacagt	agtggtgcat	ctgggtccttg	ccgcctgaga	gccccaggag	acatcgggcta											1118	
gagtgaccat	ggctatgctc	ccgtctggaa	gatgccagca	tctggcctcc	cacttttttc											1178	
agctgtgtcc	cccagtcctg	gtcttttttag	aatgtgaatg	atgataaagt	tgtgaaataa											1238	
aggtttctat	ctagttttgca	aaaaaaaaaa	aaaaa													1273	

<210> 32
 <211> 345
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> SIGNAL
 <222> 1..26

 <400> 32
 Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly Cys Gly Gln Ala
 -25 -20 -15
 Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val
 -10 -5 1 5
 Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
 10 15 20
 Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
 25 30 35
 Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
 40 45 50
 Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
 55 60 65 70
 Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
 75 80 85
 Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
 90 95 100
 Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
 105 110 115
 Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
 120 125 130
 Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
 135 140 145 150
 Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
 155 160 165
 Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
 170 175 180
 Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
 185 190 195
 Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
 200 205 210
 Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
 215 220 225 230
 Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
 235 240 245
 Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
 250 255 260
 Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
 265 270 275
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 280 285 290
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 295 300 305 310
 Gly Pro Lys Lys Gly Gly Gly Ser Lys
 315

<210> 33
 <211> 723
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..72

<220>
 <221> CDS
 <222> 73..672

<220>
 <221> 3'UTR
 <222> 673..723

<220>
 <221> polyA_signal
 <222> 689..694

<220>
 <221> polyA_site
 <222> 708..723

<400> 33
 acaagaaaag aacatggtct agactgaagt accaactaaa tcattctcctt tcaaattatc 60
 accgacacca tc atg gat tca agc acc gca cac agt ccg gtg ttt ctg gta 111
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val
 1 5 10
 ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt tca 159
 Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser
 15 20 25
 gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct aga 207
 Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg
 30 35 40 45
 aaa atg aaa atc tta ggg act atc cag atc ctg ttt gga att atg acc 255
 Lys Met Lys Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr
 50 55 60
 ttt tct ttt gga gtt atc ttc ctt ttc acc ttg tta aaa cca tat cca 303
 Phe Ser Phe Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro
 65 70 75
 agg ttt ccc ttt ata ttt ctt tca gga tat cca ttc tgg ggc tct gtt 351
 Arg Phe Pro Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val
 80 85 90
 ttg ttc att aat tct gga gcc ttc cta att gca gtg aaa aga aaa acc 399
 Leu Phe Ile Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr
 95 100 105
 aca gaa act ctg ata ata ttg agc cga ata atg aat ttt ctt agt gcc 447
 Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
 110 115 120 125
 ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta 495
 Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu
 130 135 140
 gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag 543
 Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys
 145 150 155
 gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc 591
 Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
 160 165 170
 agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc 639
 Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
 175 180 185
 cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata 692

His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
 190 195 200
 aagatgtggtt aaaataaaaa aaaaaaaaaa t

723

<210> 34
 <211> 200
 <212> PRT
 <213> Homo sapiens

<400> 34
 Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
 1 5 10 15
 Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
 20 25 30
 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
 35 40 45
 Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
 50 55 60
 Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
 65 70 75 80
 Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
 85 90 95
 Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
 100 105 110
 Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
 115 120 125
 Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
 130 135 140
 Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
 145 150 155 160
 Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
 165 170 175
 Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
 180 185 190
 Asp Cys Asp Cys Glu Gln Cys Cys
 195 200

<210> 35
 <211> 845
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..118

<220>
 <221> CDS
 <222> 119..655

<220>
 <221> 3'UTR
 <222> 656..845

<220>
 <221> polyA_signal
 <222> 809..814

<220>
 <221> polyA_site

<222> 830..845

<400> 35

```
acaaatagcc ccgatatct gtgttaccag ccttgtctcg gccacctcaa ggataatcac 60
taaattctgc caaaaggact gaggaacggt gcctggaaaaa gggcaagaat atcacggc 118
atg ggc atg agt agc ttg aaa ctg ctg aag tat gtc ctg ttt ttc ttc 166
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
aac ttg ctc ttt tgg atc tgt ggc tgc tgc att ttg ggc ttt ggg atc 214
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
tac ctg ctg atc cac aac aac ttc gga gtg ctc ttc cat aac ctc ccc 262
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
tcc ctc acg ctg ggc aat gtg ttt gtc atc gtg ggc tct att atc atg 310
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60
gta gtt gcc ttc ctg ggc tgc atg ggc tct atc aag gaa aac aag tgt 358
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
ctg ctt atg tcg ttc ttc atc ctg ctg ctg att atc ctc ctt gct gag 406
Leu Leu Met Ser Phe Phe Ile Leu Leu Leu Ile Ile Leu Leu Ala Glu
85 90 95
gtg acc ttg gcc atc ctg ctc ttt gtg gct aag ggt ctg acc gac agc 454
Val Thr Leu Ala Ile Leu Leu Phe Val Ala Lys Gly Leu Thr Asp Ser
100 105 110
atc cac cgt tac cac tca gac aat agc acc aag gca gcg tgg gac tcc 502
Ile His Arg Tyr His Ser Asp Asn Ser Thr Lys Ala Ala Trp Asp Ser
115 120 125
atc cag tca ttt ctg cag tgt tgt ggt ata aat ggc acg agt gat tgg 550
Ile Gln Ser Phe Leu Gln Cys Cys Gly Ile Asn Gly Thr Ser Asp Trp
130 135 140
acc agt ggc cca cca gca tct tgc ccc tca gat cga aaa gtg gag ggt 598
Thr Ser Gly Pro Pro Ala Ser Cys Pro Ser Asp Arg Lys Val Glu Gly
145 150 155 160
tgc tat gcg aaa gca aga ctg tgg ttt cat tcc aat ttc ttt att aga 646
Cys Tyr Ala Lys Ala Arg Leu Trp Phe His Ser Asn Phe Phe Ile Arg
165 170 175
ggg cct tat tgatgtgttc taagtctttc cagaaaaaaa ctatccagtg 695
Gly Pro Tyr
atztatatcc tgatttcaac cagtcactta gctgataatc acagtaagaa gacttctggt 755
attatctctc tatcagataa gattttgtta atgtactatt ttactcttca ataaataaaa 815
cagtttatta tcgcaaaaaa aaaaaaaaaa 845
```

<210> 36

<211> 179

<212> PRT

<213> Homo sapiens

<400> 36

```
Met Gly Met Ser Ser Leu Lys Leu Leu Lys Tyr Val Leu Phe Phe Phe
1 5 10 15
Asn Leu Leu Phe Trp Ile Cys Gly Cys Cys Ile Leu Gly Phe Gly Ile
20 25 30
Tyr Leu Leu Ile His Asn Asn Phe Gly Val Leu Phe His Asn Leu Pro
35 40 45
Ser Leu Thr Leu Gly Asn Val Phe Val Ile Val Gly Ser Ile Ile Met
50 55 60
Val Val Ala Phe Leu Gly Cys Met Gly Ser Ile Lys Glu Asn Lys Cys
65 70 75 80
```



```

<400> 38
Met Ser Pro Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val
1          5          10          15
Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala
          20          25          30
Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys Glu Glu Asn Ala
          35          40          45
Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly Ser Lys Thr Ala Leu
          50          55          60
Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile
65          70          75          80
Ala

```

```

<210> 39
<211> 1816
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..259

```

```

<220>
<221> CDS
<222> 260..1048

```

```

<220>
<221> 3'UTR
<222> 1049..1816

```

```

<220>
<221> polyA_signal
<222> 1782..1787

```

```

<220>
<221> polyA_site
<222> 1801..1816

```

```

<400> 39
actctggggc cattgccagc cggctgtagg cattcagggc agtgtcttct gcatctccta 60
ggaacctcgg gagcggcagc tccggcgccct ggtagcgaga ggcgggttcc ggagatcccg 120
gcctcacttc gtcccactgt ggtaggggt gagtcctgcg aatgttaagt gatttgc tca 180
aggcgcccat ttgcgaggaa ttggagccca ggccagttct ctgagcctat cattagggct 240
aaaggagtgc gtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc ctg 292
          Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu
          -15          -10
ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac tgg 340
Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp
          -5          1          5
atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac atg 388
Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met
          10          15          20
ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc tat 436
Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe Tyr
          25          30          35          40
gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tcg tgg gtg ggg ccc 484
Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro
          45          50          55
aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc ttc 532
Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala Phe

```

	60		65		70	
gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac cat	580					
Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn His						
75	80	85				
gga agg act gcc aac ctg tac tcc ctt cac agc tgg ctg ggc atc acc	628					
Gly Arg Thr Ala Asn Leu Ser Leu His Ser Trp Leu Gly Ile Thr						
90	95	100				
act gtc ttc ctg ttc ggc tgc cag tgg ttc ctg ggc ttt gct gtc ttc	676					
Thr Val Phe Leu Phe Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe						
105	110	115	120			
ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctg cta aaa cct atc	724					
Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile						
125	130	135				
cac gtc ttt ttt gga gcc gcc atc ctg tct ctg tcc atc gca tcc gtc	772					
His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val						
140	145	150				
att tgc ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc acc	820					
Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr						
155	160	165				
agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc acc	868					
Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr						
170	175	180				
ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctg tac atc ctt ctg	916					
Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu						
185	190	195	200			
gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga cag	964					
Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln						
205	210	215				
ctg ctg cta cag ctg agg cct gga tcc cgg cct ttc cct gtg act tac	1012					
Leu Leu Leu Gln Leu Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr						
220	225	230				
gtg tct gtc acc ggc agg cag ccc tac aaa tcc tgg tgacctgtc	1058					
Val Ser Val Thr Gly Arg Gln Pro Tyr Lys Ser Trp						
235	240					
tcccaagaac agagcctgtc cccagatgtc ccagtagcga tgagtaacag aggtggctgt	1118					
ggacttcttc tacttctcct tgctggatca gggccttctt gcctcccgtt gggcagggtct	1178					
ggccttgctc tcttggcagg gccccagccc ctctgaccac tctgcagctc accatgcagc	1238					
tgatgcaaaa gttgtgggtgt ccagtgtgca gcagccctgg gagccactgc caccttcaga	1298					
gggggttcctt gctgagaccc acattgcttc acctggcccc accatggctg cttgcctggc	1358					
ccaacctagc gttctgtgcc atgctagaac ttgagctgtt gctcttcttc aggggaggaa	1418					
atagggtgga gagcggaag ggtcttgctc ctaagtgttg ctgctgtggc ttttttgctt	1478					
tctccaaaga cgcactgcca ggtcccaagc ttcagactgc tgtgcttagt aagcaagtga	1538					
gaagcctggg gtttgagcc cacctactct ctggcagcat cagcatccta ctccggcaa	1598					
catcaggcca acgtccaccc cagcctcaca ttgccagatg ttggcagaag ggctaattatt	1658					
gaccgtcttg actggctgga gccttcaaag ccactgggat gtcctccagg cacctgggtc	1718					
ccatgaccag ctccccgtct ccataggggt aggcatttca ctggtttatg aagctcgagt	1778					
ttcattaaat atgttaagaa tcaaaaaaaaa aaaaaaaaa	1816					

<210> 40
 <211> 263
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..20

<400> 40
 Met Val Ser Gly Arg Phe Tyr Leu Ser Cys Leu Leu Leu Gly Ser Leu
 -20 -15 -10 -5

Gly Ser Met Cys Ile Leu Phe Thr Ile Tyr Trp Met Gln Tyr Trp Arg
 1 5 10
 Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr Met Phe Asn Trp His Pro
 15 20 25
 Val Leu Met Val Ala Gly Met Val Val Phe Tyr Gly Gly Ala Ser Leu
 30 35 40
 Val Tyr Arg Leu Pro Gln Ser Trp Val Gly Pro Lys Leu Pro Trp Lys
 45 50 55 60
 Leu Leu His Ala Ala Leu His Leu Met Ala Phe Val Leu Thr Val Val
 65 70 75
 Gly Leu Val Ala Val Phe Thr Phe His Asn His Gly Arg Thr Ala Asn
 80 85 90
 Leu Tyr Ser Leu His Ser Trp Leu Gly Ile Thr Thr Val Phe Leu Phe
 95 100 105
 Gly Cys Gln Trp Phe Leu Gly Phe Ala Val Phe Leu Leu Pro Trp Ala
 110 115 120
 Ser Met Trp Leu Arg Ser Leu Leu Lys Pro Ile His Val Phe Phe Gly
 125 130 135 140
 Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser Val Ile Ser Gly Ile Asn
 145 150 155
 Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr Thr Arg Pro Tyr His Ser
 160 165 170
 Leu Pro Ser Glu Ala Val Phe Ala Asn Ser Thr Gly Met Leu Val Val
 175 180 185
 Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu Leu Ala Ser Ser Trp Lys
 190 195 200
 Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg Gln Leu Leu Gln Leu
 205 210 215 220
 Arg Pro Gly Ser Arg Pro Phe Pro Val Thr Tyr Val Ser Val Thr Gly
 225 230 235
 Arg Gln Pro Tyr Lys Ser Trp
 240

<210> 41
 <211> 643
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..90

<220>
 <221> CDS
 <222> 91..462

<220>
 <221> 3'UTR
 <222> 463..643

<220>
 <221> polyA_signal
 <222> 607..612

<220>
 <221> polyA_site
 <222> 628..643

<400> 41
 acccctaccc cagcggccct cccgcgcgcg cgggttaaata cccgcacctg agcatcggct 60

<212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..227

<220>
 <221> CDS
 <222> 228..501

<400> 43
 actcttactc tttctctctc actctctctc ttttcccacc cttaagccaa gtacagggat 60
 agttgtctca tcattggtgg cttaaaatga tgtttttgaa caagaagaca ccccatggga 120
 ctgatctcaa atgcagctgt gactaaaacc tctaggtgct gtgctgtcct gaggcctggg 180
 ccatggtgcc caaggaaagc ccctgaagct caccaggagg aagaagc atg cag ggc 236
 Met Gln Gly
 -30
 act cct gga ggc ggg acg cgc cct ggg cca tcc ccc gtg gac agg cgg 284
 Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val Asp Arg Arg
 -25 -20 -15
 aca ctc ctg gtc ttc agc ttt atc ctg gca gca gct ttg ggc caa atg 332
 Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu Gly Gln Met
 -10 -5 1
 aat ttc aca ggg gac cag gtt ctt cga gtc ctg gcc aaa gat gag aag 380
 Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys Asp Glu Lys
 5 10 15
 cag ctt tca ctt ctc ggg gat ctg gag ggc ctg aaa ccc cag aag gtg 428
 Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro Gln Lys Val
 20 25 30 35
 gac ttc tgg cgt ggc cca gcc agg ccc agc ctc cct gtg gat atg aga 476
 Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val Asp Met Arg
 40 45 50
 gtt cct ttc tcc gaa ctg aaa gac a
 Val Pro Phe Ser Glu Leu Lys Asp 501
 55

<210> 44
 <211> 91
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..33

<400> 44
 Met Gln Gly Thr Pro Gly Gly Gly Thr Arg Pro Gly Pro Ser Pro Val
 -30 -25 -20
 Asp Arg Arg Thr Leu Leu Val Phe Ser Phe Ile Leu Ala Ala Ala Leu
 -15 -10 -5
 Gly Gln Met Asn Phe Thr Gly Asp Gln Val Leu Arg Val Leu Ala Lys
 1 5 10 15
 Asp Glu Lys Gln Leu Ser Leu Leu Gly Asp Leu Glu Gly Leu Lys Pro
 20 25 30
 Gln Lys Val Asp Phe Trp Arg Gly Pro Ala Arg Pro Ser Leu Pro Val
 35 40 45
 Asp Met Arg Val Pro Phe Ser Glu Leu Lys Asp
 50 55

<210> 45
 <211> 960
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..97

<220>
 <221> CDS
 <222> 98..934

<220>
 <221> 3'UTR
 <222> 935..960

<400> 45
 ataatcacct ctcattccag actatgtag gtcttaatgg tgggaggacg cccgagtgt 60
 cggcccgttt caccgccagg aggaaggaca ctgggtc atg acg cca tca gaa ggc 115
 Met Thr Pro Ser Glu Gly
 1 5
 gcc aga gca ggg acc gga cgc gag ttg gag atg ttg gac tcg ctg ttg 163
 Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu Met Leu Asp Ser Leu Leu
 10 15 20
 gcc ttg ggc ggc ctg gtg ctg ctt cgg gat tcc gtg gag tgg gag ggg 211
 Ala Leu Gly Gly Leu Val Leu Leu Arg Asp Ser Val Glu Trp Glu Gly
 25 30 35
 cgc agt ctc ttg aag gcg ctt gtc aag aaa tct gca ctg tgt ggg gag 259
 Arg Ser Leu Leu Lys Ala Leu Val Lys Lys Ser Ala Leu Cys Gly Glu
 40 45 50
 caa gtg cat atc ctg ggc tgt gaa gtg agc gag gaa gag ttt cgt gaa 307
 Gln Val His Ile Leu Gly Cys Glu Val Ser Glu Glu Glu Phe Arg Glu
 55 60 65 70
 ggt ttt gac tct gat atc aac aat cgg ctg gtt tac cat gac ttc ttc 355
 Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu Val Tyr His Asp Phe Phe
 75 80 85
 aga gac cct ctc aac tgg tca aaa act gag gag gcc ttt cct ggg ggg 403
 Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu Glu Ala Phe Pro Gly Gly
 90 95 100
 ccg ctg gga gcc ttg aga gcc atg tgc aag agg aca gat cct gtt cct 451
 Pro Leu Gly Ala Leu Arg Ala Met Cys Lys Arg Thr Asp Pro Val Pro
 105 110 115
 gtc acc att gct ctc gat tca ctc agc tgg ctg cta ctt cgc ctt ccc 499
 Val Thr Ile Ala Leu Asp Ser Leu Ser Trp Leu Leu Arg Leu Pro
 120 125 130
 tgc acc aca ctc tgc cag gtc ctg cat gct gtg agc cat cag gac tct 547
 Cys Thr Thr Leu Cys Gln Val Leu His Ala Val Ser His Gln Asp Ser
 135 140 145 150
 tgt cct ggt gac agc tcc tca gtg ggg aaa gtg agt gtg ctg ggc ttg 595
 Cys Pro Gly Asp Ser Ser Ser Val Gly Lys Val Ser Val Leu Gly Leu
 155 160 165
 cta cat gaa gag ctt cat gga cca ggc cct gtg gga gct ctc agc agc 643
 Leu His Glu Glu Leu His Gly Pro Gly Pro Val Gly Ala Leu Ser Ser
 170 175 180
 ctt gct cag act gag gtg acc ctg ggc ggt acc atg ggc cag gcc tcg 691
 Leu Ala Gln Thr Glu Val Thr Leu Gly Gly Thr Met Gly Gln Ala Ser
 185 190 195
 gcc cac atc ctg tgt cgg agg ccc cga cag cgc cca act gac cag act 739
 Ala His Ile Leu Cys Arg Arg Pro Arg Gln Arg Pro Thr Asp Gln Thr

200	205	210	
cag tgg ttc tcc atc ctt ccg gac ttc agc ctg gat ctc caa gag ggg			787
Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser Leu Asp Leu Gln Glu Gly			
215	220	225	230
ccc tct gta gag tcc cag ccc tac tcc gat cct cat ata ccc ccg gta			835
Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp Pro His Ile Pro Pro Val			
235	240	245	
tct aag aat gcc aag gcc aga aca agg aaa tgt agt tta gta tct ggt			883
Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys Cys Ser Leu Val Ser Gly			
250	255	260	
cac ggg aga gaa aat aaa agc tgc aga ggt tgg ggg tgg ggt cag gga			931
His Gly Arg Glu Asn Lys Ser Cys Arg Gly Trp Gly Trp Gly Gln Gly			
265	270	275	
ttc tagggatggg gcagagtggc agcatc			960
Phe			

<210> 46
 <211> 279
 <212> PRT
 <213> Homo sapiens

<400> 46

Met Thr Pro Ser Glu Gly Ala Arg Ala Gly Thr Gly Arg Glu Leu Glu	
1	15
Met Leu Asp Ser Leu Leu Ala Leu Gly Gly Leu Val Leu Leu Arg Asp	
20	30
Ser Val Glu Trp Glu Gly Arg Ser Leu Leu Lys Ala Leu Val Lys Lys	
35	45
Ser Ala Leu Cys Gly Glu Gln Val His Ile Leu Gly Cys Glu Val Ser	
50	60
Glu Glu Glu Phe Arg Glu Gly Phe Asp Ser Asp Ile Asn Asn Arg Leu	
65	80
Val Tyr His Asp Phe Phe Arg Asp Pro Leu Asn Trp Ser Lys Thr Glu	
85	95
Glu Ala Phe Pro Gly Gly Pro Leu Gly Ala Leu Arg Ala Met Cys Lys	
100	110
Arg Thr Asp Pro Val Pro Val Thr Ile Ala Leu Asp Ser Leu Ser Trp	
115	125
Leu Leu Leu Arg Leu Pro Cys Thr Thr Leu Cys Gln Val Leu His Ala	
130	140
Val Ser His Gln Asp Ser Cys Pro Gly Asp Ser Ser Ser Val Gly Lys	
145	160
Val Ser Val Leu Gly Leu Leu His Glu Glu Leu His Gly Pro Gly Pro	
165	175
Val Gly Ala Leu Ser Ser Leu Ala Gln Thr Glu Val Thr Leu Gly Gly	
180	190
Thr Met Gly Gln Ala Ser Ala His Ile Leu Cys Arg Arg Pro Arg Gln	
195	205
Arg Pro Thr Asp Gln Thr Gln Trp Phe Ser Ile Leu Pro Asp Phe Ser	
210	220
Leu Asp Leu Gln Glu Gly Pro Ser Val Glu Ser Gln Pro Tyr Ser Asp	
225	235
Pro His Ile Pro Pro Val Ser Lys Asn Ala Lys Ala Arg Thr Arg Lys	
245	255
Cys Ser Leu Val Ser Gly His Gly Arg Glu Asn Lys Ser Cys Arg Gly	
260	270
Trp Gly Trp Gly Gln Gly Phe	
275	

<210> 47

<211> 1294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..266

<220>
 <221> CDS
 <222> 267..1139

<220>
 <221> 3'UTR
 <222> 1140..1294

<220>
 <221> polyA_signal
 <222> 1246..1251

<220>
 <221> polyA_site
 <222> 1279..1294

<400> 47
 gactctgagg ctcctctcttt gctctaacag acagcagcga ctttaggctg gataatagtc 60
 aaattcttac ctcgctcttt cactgctagt aagatcagat tgcgtttctt tcagttactc 120
 ttcaatcgcc agtttcttga tctgcttcta aaagaagaag tagagaagat aaatcctgtc 180
 ttcaatacct ggaaggaaaa acaaaataac ctcaactcgg ttttgaaaaa aacattccaa 240
 gaactttcat cagagatttt acttag atg att tac aca atg aag aaa gta cat 293
 Met Ile Tyr Thr Met Lys Lys Val His
 -25 -20
 gca ctt tgg gct tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct 341
 Ala Leu Trp Ala Ser Val Cys Leu Leu Asn Leu Ala Pro Ala Pro
 -15 -10 -5
 ctt aat gct gat tct gag gaa gat gaa gaa cac aca att atc aca gat 389
 Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
 1 5 10
 acg gag ttg cca cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag 437
 Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
 15 20 25 30
 gcg gat gat ggc cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat 485
 Ala Asp Asp Gly Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
 35 40 45
 att ttc act cga cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga 533
 Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
 50 55 60
 aat cag aat cga ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca 581
 Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr
 65 70 75
 aga gaa aag cca gat ttc tgc ttt ttg gaa gaa gat cct gga ata tgt 629
 Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys
 80 85 90
 cga ggt tat att acc agg tat ttt tat aac aat cag aca aaa cag tgt 677
 Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys Gln Cys
 95 100 105 110
 gaa cgt ttc aag tat ggt gga tgc ctg ggc aat atg aac aat ttt gag 725
 Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly Asn Met Asn Asn Phe Glu
 115 120 125
 aca ctg gaa gaa tgc aag aac att tgt gaa gat ggt ccg aat ggt ttc 773

Thr	Leu	Glu	Glu	Cys	Lys	Asn	Ile	Cys	Glu	Asp	Gly	Pro	Asn	Gly	Phe		
			130					135					140				
cag	gtg	gat	aat	tat	gga	acc	cag	ctc	aat	gct	gtg	aat	aac	tcc	ctg	821	
Gln	Val	Asp	Asn	Tyr	Gly	Thr	Gln	Leu	Asn	Ala	Val	Asn	Asn	Ser	Leu		
		145					150					155					
act	ccg	caa	tca	acc	aag	gtt	ccc	agc	ctt	ttt	gaa	ttt	cac	ggg	ccc	869	
Thr	Pro	Gln	Ser	Thr	Lys	Val	Pro	Ser	Leu	Phe	Glu	Phe	His	Gly	Pro		
	160					165					170						
tca	tgg	tgt	ctc	act	cca	gca	gac	aga	gga	ttg	tgt	cgt	gcc	aat	gag	917	
Ser	Trp	Cys	Leu	Thr	Pro	Ala	Asp	Arg	Gly	Leu	Cys	Arg	Ala	Asn	Glu		
175					180				185					190			
aac	aga	ttc	tac	tac	aat	tca	gtc	att	ggg	aaa	tgc	cgc	cca	ttt	aag	965	
Asn	Arg	Phe	Tyr	Tyr	Asn	Ser	Val	Ile	Gly	Lys	Cys	Arg	Pro	Phe	Lys		
			195					200					205				
tac	agt	gga	tgt	ggg	gga	aat	gaa	aac	aat	ttt	act	tcc	aaa	caa	gaa	1013	
Tyr	Ser	Gly	Cys	Gly	Gly	Asn	Glu	Asn	Asn	Phe	Thr	Ser	Lys	Gln	Glu		
		210				215						220					
tgt	ctg	agg	gca	tgt	aaa	aaa	ggg	ttc	atc	caa	aga	ata	tca	aaa	gga	1061	
Cys	Leu	Arg	Ala	Cys	Lys	Lys	Gly	Phe	Ile	Gln	Arg	Ile	Ser	Lys	Gly		
		225				230						235					
ggc	cta	att	aaa	acc	aaa	aga	aaa	aga	aag	aag	cag	aga	gtg	aaa	ata	1109	
Gly	Leu	Ile	Lys	Thr	Lys	Arg	Lys	Arg	Lys	Lys	Gln	Arg	Val	Lys	Ile		
	240				245						250						
gca	tat	gaa	gaa	att	ttt	gtt	aaa	aat	atg	tgaatttggt	atagcaatgt					1159	
Ala	Tyr	Glu	Glu	Ile	Phe	Val	Lys	Asn	Met								
255					260												
aacattaatt	ctactaaata	ttttatatga	aatgttttcac	tatgatttttc	tattttttctt	1219											
ctaaaatgct	tttaattaat	atgttcatta	aattttctat	gcttattgta	cttgttacca	1279											
aaaaaaaaaa	aaaaa					1294											

<210> 48
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..28

<400>	48																
Met	Ile	Tyr	Thr	Met	Lys	Lys	Val	His	Ala	Leu	Trp	Ala	Ser	Val	Cys		
			-25					-20					-15				
Leu	Leu	Leu	Asn	Leu	Ala	Pro	Ala	Pro	Leu	Asn	Ala	Asp	Ser	Glu	Glu		
		-10					-5					1					
Asp	Glu	Glu	His	Thr	Ile	Ile	Thr	Asp	Thr	Glu	Leu	Pro	Pro	Leu	Lys		
5				10					15						20		
Leu	Met	His	Ser	Phe	Cys	Ala	Phe	Lys	Ala	Asp	Asp	Gly	Pro	Cys	Lys		
			25					30					35				
Ala	Ile	Met	Lys	Arg	Phe	Phe	Phe	Asn	Ile	Phe	Thr	Arg	Gln	Cys	Glu		
		40						45					50				
Glu	Phe	Ile	Tyr	Gly	Gly	Cys	Glu	Gly	Asn	Gln	Asn	Arg	Phe	Glu	Ser		
	55					60						65					
Leu	Glu	Glu	Cys	Lys	Lys	Met	Cys	Thr	Arg	Glu	Lys	Pro	Asp	Phe	Cys		
	70					75					80						
Phe	Leu	Glu	Glu	Asp	Pro	Gly	Ile	Cys	Arg	Gly	Tyr	Ile	Thr	Arg	Tyr		
85					90					95					100		
Phe	Tyr	Asn	Asn	Gln	Thr	Lys	Gln	Cys	Glu	Arg	Phe	Lys	Tyr	Gly	Gly		
			105					110						115			
Cys	Leu	Gly	Asn	Met	Asn	Asn	Phe	Glu	Thr	Leu	Glu	Glu	Cys	Lys	Asn		
			120					125					130				

Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
135 140 145
Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
150 155 160
Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
165 170 175 180
Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
185 190 195
Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn
200 205 210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
215 220 225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
230 235 240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
245 250 255 260
Lys Asn Met

<210> 49
<211> 1194
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..47

<220>
<221> CDS
<222> 48..1100

<220>
<221> 3'UTR
<222> 1101..1194

<220>
<221> polyA_signal
<222> 1159..1164

<220>
<221> polyA_site
<222> 1179..1194

<400> 49
ctcctcagct tcaggcacca ccactgacct gggacagtga atcgaca atg ccg tct 56
Met Pro Ser
tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc 104
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20 -15 -10 -5
cct gtc tcc ctg ggg acc aag gct gac act cac gat gaa atc ctg gag 152
Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu
1 5 10
ggc ctg aat ttc aac ctc acg gag att ccg gag gct cag atc cat gaa 200
Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln Ile His Glu
15 20 25
ggc ttc cag gaa ctc ctc cgt acc ctc aac cag cca gac agc cag ctc 248
Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu
30 35 40
cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc ctg aag cta 296
Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu

45	50	55	60	
gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac tca gaa gcc				344
Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala				
65	70	75		
ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa cag atc aac				392
Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn				
80	85	90		
gat tac gtg gag aag ggt act caa ggg aaa att gtg gat ttg gtc aag				440
Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys				
95	100	105		
gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac atc ttc ttt				488
Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe				
110	115	120		
aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc gag gaa gag				536
Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu				
125	130	135	140	
gac ttc cac gtg gac cag gtg acc acc gtg aag gtg cct atg atg aag				584
Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys				
145	150	155		
cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg tcc agc tgg				632
Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp				
160	165	170		
gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc ttc ttc ctg				680
Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu				
175	180	185		
cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc acc cac gat				728
Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp				
190	195	200		
atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct gcc agc tta				776
Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu				
205	210	215	220	
cat tta ccc aaa ctg tcc att act gga acc tat gat ctg aag agc gtc				824
His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val				
225	230	235		
ctg ggt caa ctg ggc atc act aag gtc ttc agc aat ggg gct gac ctc				872
Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu				
240	245	250		
tcc ggg gtc aca gag gag gca ccc ctg aag ctc tcc aag gcc gtg cat				920
Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His				
255	260	265		
aag gct gtg ctg acc atc gac gag aaa ggg act gaa gct gct ggg gcc				968
Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala				
270	275	280		
atg ttt tta gag gcc ata ccc atg tct atc ccc ccc gag gtc aag ttc				1016
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe				
285	290	295	300	
aac aaa ccc ttt gtc ttc tta atg att gac caa aat acc aag tct ccc				1064
Asn Lys Pro Phe Val Phe Leu Met Ile Asp Gln Asn Thr Lys Ser Pro				
305	310	315		
ctc ttc atg gga aaa gtg gtg aat ccc acc caa aaa taactgcctc				1110
Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys				
320	325			
tcgctcctca acccctcccc tccatccctg gccccctccc tggatgacat taaagaaggg				1170
ttgagctgaa aaaaaaaaaa aaaa				1194

<210> 50
 <211> 351
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 50
 Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
 -20 -15 -10
 Cys Leu Val Pro Val Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
 -5 1 5
 Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
 10 15 20
 Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
 25 30 35 40
 Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
 45 50 55
 Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
 60 65 70
 Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
 75 80 85
 Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp
 90 95 100
 Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr
 105 110 115 120
 Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr
 125 130 135
 Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val Pro
 140 145 150
 Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu
 155 160 165
 Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile
 170 175 180
 Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu
 185 190 195 200
 Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser
 205 210 215
 Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu
 220 225 230
 Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly
 235 240 245
 Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
 250 255 260
 Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala
 265 270 275 280
 Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu
 285 290 295
 Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Asp Gln Asn Thr
 300 305 310
 Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr Gln Lys
 315 320 325

<210> 51
 <211> 1317
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..289

<220>

<221> CDS

<222> 290..1162

<220>

<221> 3'UTR

<222> 1163..1317

<220>

<221> polyA_signal

<222> 1269..1274

<220>

<221> polyA_site

<222> 1302..1317

<400> 51

```
aactgccagt gatctctgaa gccgactctg aggctccctc tttgctctaa cagacagcag 60
cgacttttagg ctggataata gtcaaattct tacctcgctc tttcactgct agtaagatca 120
gattgcgttt ctttcagtta ctcttcaatc gccagtttct tgatctgctt ctaaaagaag 180
aagtagagaa gataaatcct gtcttcaata cctggaagga aaaacaaaat aacctcaact 240
ccgttttgaa aaaaacattc caagaacttt catcagagat tttacttag atg att tac 298
                                     Met Ile Tyr
                                     -25
aca atg aag aaa gta cat gca ctt tgg gct tct gta tgc ctg ctg ctt 346
Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys Leu Leu Leu
                                     -20
aat ctt gcc cct gcc cct ctt aat gct gat tct gag gaa gat gaa gaa 394
Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu
                                     -5
cac aca att atc aca gat acg gag ttg cca cca ctg aaa ctt atg cat 442
His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys Leu Met His
                                     10
tca ttt tgt gca ttc aag tgc gat gat ggc cca tgt aaa gca atc atg 490
Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys Ala Ile Met
                                     25
aaa aga ttt ttc ttc aat att ttc act cga cag tgc gaa gaa ttt ata 538
Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile
                                     45
tat ggg gga tgt gaa gga aat cag aat cga ttt gaa agt ctg gaa gag 586
Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu
                                     60
tgc aaa aaa atg tgt aca aga gaa aag cca gat ttc tgc ttt ttg gaa 634
Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys Phe Leu Glu
                                     75
gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat aac 682
Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
                                     90
aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga tgc ctg ggc 730
Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
                                     105
aat atg aac aat ttt gag aca ctg gaa gaa tgc aag aac att tgt gaa 778
Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn Ile Cys Glu
                                     125
gat ggt ccg aat ggt ttc cag gtg gat aat tat gga acc cag ctc aat 826
Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr Gln Leu Asn
                                     140
gct gtg aat aac tcc ctg act ccg caa tca acc aag gtt ccc agc ctt 874
Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val Pro Ser Leu
                                     155
ttt gaa ttt cac ggt ccc tca tgg tgt ctc act cca gca gac aga gga 922
                                     160
                                     165
```


Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala Asp Arg Gly
 170 175 180
 ttg tgt cgt gcc aat gag aac aga ttc tac tac aat tca gtc att ggg 970
 Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser Val Ile Gly
 185 190 195 200
 aaa tgc cgc cca ttt aag tac agt gga tgt ggg gga aat gaa aac aat 1018
 Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn Glu Asn Asn
 205 210 215
 ttt act tcc aaa caa gaa tgt ctg agg gca tgt aaa aaa ggt ttc atc 1066
 Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys Gly Phe Ile
 220 225 230
 caa aga ata tca aaa gga ggc cta att aaa acc aaa aga aaa aga aag 1114
 Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg Lys Arg Lys
 235 240 245
 aag cag aga gtg aaa ata gca tat gaa gaa att ttt gtt aaa aat atg 1162
 Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val Lys Asn Met
 250 255 260
 tgaatttggt atagcaatgt aacattaatt ctactaaata ttttatatga aatgtttcac 1222
 tatgattttc tattttttctt ctaaaatgct ttttaattaat atgttcatta aattttctat 1282
 gcttattgta cttgttatca aaaaaaaaaa aaaaa 1317

<210> 52
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..28

<400> 52
 Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
 -25 -20 -15
 Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
 -10 -5 1
 Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
 5 10 15 20
 Leu Met His Ser Phe Cys Ala Phe Lys Ser Asp Asp Gly Pro Cys Lys
 25 30 35
 Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
 40 45 50
 Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
 55 60 65
 Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Glu Lys Pro Asp Phe Cys
 70 75 80
 Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
 85 90 95 100
 Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
 105 110 115
 Cys Leu Gly Asn Met Asn Asn Phe Glu Thr Leu Glu Glu Cys Lys Asn
 120 125 130
 Ile Cys Glu Asp Gly Pro Asn Gly Phe Gln Val Asp Asn Tyr Gly Thr
 135 140 145
 Gln Leu Asn Ala Val Asn Asn Ser Leu Thr Pro Gln Ser Thr Lys Val
 150 155 160
 Pro Ser Leu Phe Glu Phe His Gly Pro Ser Trp Cys Leu Thr Pro Ala
 165 170 175 180
 Asp Arg Gly Leu Cys Arg Ala Asn Glu Asn Arg Phe Tyr Tyr Asn Ser
 185 190 195
 Val Ile Gly Lys Cys Arg Pro Phe Lys Tyr Ser Gly Cys Gly Gly Asn

```

      200      205      210
Glu Asn Asn Phe Thr Ser Lys Gln Glu Cys Leu Arg Ala Cys Lys Lys
      215      220      225
Gly Phe Ile Gln Arg Ile Ser Lys Gly Gly Leu Ile Lys Thr Lys Arg
      230      235      240
Lys Arg Lys Lys Gln Arg Val Lys Ile Ala Tyr Glu Glu Ile Phe Val
      245      250      255      260
Lys Asn Met

<210> 53
<211> 1907
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..1043

<220>
<221> CDS
<222> 1044..1664

<220>
<221> 3'UTR
<222> 1665..1907

<220>
<221> polyA_signal
<222> 1869..1874

<220>
<221> polyA_site
<222> 1892..1907

<400> 53
caaaaaaatt ctaggtcatg atccccataa atgaagagtg atcagtccaa tcccagggaa 60
cctggacatt ttgggtattg tttcagtgga acatgccttt cataagttcc attttcttgg 120
gtatctctta ggaagcaagc ataggaaaca ggcccatccg tctgcctgtt ttgcttcttc 180
atctcacttc tacacgaggg tgctgtgct caattgctgt tttcccctaa agagactctt 240
ttccataagt ttgtgaaatg ccatcgacaa acctgatcgc attgcatttc actctgctgt 300
tgagtcgatt tttcttttatt ttatcattta gtaactcctt gctctacaga gctttcacct 360
tccacatatt tcagattcat tctttcctaa actatgtggt ggtctacgtc ctactgact 420
tatcaacatg ctaccatcat gcacttccta tctctattcc tcttctttta atttgggtcc 480
aaatggctca caccattatt ctgagctatt acctgcctac gcagtcctag aaagtaagtg 540
attcaggaaa cattccccaa aagtaaagtt tctcaggtaa gatcagaaga ctcccatgag 600
tactgctgc tcaggatcac atctggctcc ttgaagagtg attcatcaga cttacatag 660
atcttgctcat aaaaatgaaa gaggcctcgg gggaaggtct tgggctggtg gcttctgttg 720
gagtcctggg ctgtgggggtg aaagccgtgg ctgtagagct tcatgaggag ttacttagct 780
ttgctctcct gtggacaggc catgcctgtg cctcccccaa gcacgcgaaa aattggcata 840
gatgggccct tctcaaaaat cccactcctg gagcactggc caaaattact accatcctga 900
tgctgggctt gcagtccttt cctttgggaa tatgaacatg gtcaaaatta agtgaacgtg 960
tctttctggc tttctgtaca atggagcaga acaaagtatc aatttaacta aaatttgaac 1020
taaatcctct ttccagggtt gga atg cac ttc tgt gga ggc acc ttg ata tcc 1073
Met His Phe Cys Gly Gly Thr Leu Ile Ser
      1      5      10
cca gag tgg gtg ttg act gct gcc cac tgc ttg gag aag tcc cca agg 1121
Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu Glu Lys Ser Pro Arg
      15      20      25
cct tca tcc tac aag gtc atc ctg ggt gca cac caa gaa gtg aat ctc 1169
Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His Gln Glu Val Asn Leu

```

	30		35		40		
gaa ccg cat gtt cag gaa ata gaa gtg tct agg ctg ttc ttg gag ccc						1217	
Glu Pro His Val Gln Glu Ile Glu Val Ser Arg Leu Phe Leu Glu Pro							
	45		50		55		
aca cga aaa gat att gcc ttg cta aag cta agc agt cct gcc gtc atc						1265	
Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser Ser Pro Ala Val Ile							
	60		65		70		
act gac aaa gta atc cca gct tgt ctg cca tcc cca aat tat gtg gtc						1313	
Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser Ser Pro Asn Tyr Val Val							
	75		80		85		90
gct gac cgg acc gaa tgt ttc atc act ggc tgg gga gaa acc caa ggt						1361	
Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly							
	95		100		105		
act ttt gga gct ggc ctt ctc aag gaa gcc cag ctc cct gtg att gag						1409	
Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln Leu Pro Val Ile Glu							
	110		115		120		
aat aaa gtg tgc aat cgc tat gag ttt ctg aat gga aga gtc caa tcc						1457	
Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser							
	125		130		135		
acc gaa ctc tgt gct ggg cat ttg gcc gga ggc act gac agt tgc cag						1505	
Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly Thr Asp Ser Cys Gln							
	140		145		150		
ggt gac agt gga ggt cct ctg gtt tgc ttc gag aag gac aaa tac att						1553	
Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile							
	155		160		165		170
tta caa gga gtc act tct tgg ggt ctt ggc tgt gca cgc ccc aat aag						1601	
Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys							
	175		180		185		
cct ggt gtc tat gtt cgt gtt tca agg ttt gtt act tgg att gag gga						1649	
Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val Thr Trp Ile Glu Gly							
	190		195		200		
gtg atg aga aat aat taattggacg ggagacagag tgacgcactg actcacctag						1704	
Val Met Arg Asn Asn							
	205						
aggctggaac gtgggtagggt atttagcatg ctggaaataa ctggcagtaa tcaaacgaag						1764	
acactgtccc cagctaccag ctatgccaaa cctcggcatt ttttgtgtta ttttctgact						1824	
gctggattct gtagtaagggt gacatagcta tgacatttgt taaaaataaa ctctgtactt						1884	
aactttgaaa aaaaaaaaaa aaa						1907	

<210> 54
 <211> 207
 <212> PRT
 <213> Homo sapiens

<400> 54
 Met His Phe Cys Gly Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr
 1 5 10 15
 Ala Ala His Cys Leu Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val
 20 25 30
 Ile Leu Gly Ala His Gln Glu Val Asn Leu Glu Pro His Val Gln Glu
 35 40 45
 Ile Glu Val Ser Arg Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala
 50 55 60
 Leu Leu Lys Leu Ser Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro
 65 70 75 80
 Ala Cys Leu Pro Ser Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys
 85 90 95
 Phe Ile Thr Gly Trp Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu
 100 105 110
 Leu Lys Glu Ala Gln Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg

115 120 125
 Tyr Glu Phe Leu Asn Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly
 130 135 140
 His Leu Ala Gly Gly Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 145 150 155 160
 Leu Val Cys Phe Glu Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser
 165 170 175
 Trp Gly Leu Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg
 180 185 190
 Val Ser Arg Phe Val Thr Trp Ile Glu Gly Val Met Arg Asn Asn
 195 200 205

<210> 55
 <211> 809
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..25

<220>
 <221> CDS
 <222> 26..628

<220>
 <221> 3'UTR
 <222> 629..809

<220>
 <221> polyA_signal
 <222> 766..771

<220>
 <221> polyA_site
 <222> 795..809

<400> 55
 agaaagggtgt gggtggcatg gggca atg ctt gag gta tca gat gca ctg gga 52
 Met Leu Glu Val Ser Asp Ala Leu Gly
 1 5
 gga cct gga aga gta cca ggg gcc aca gca ggg atg aat gga gtg gac 100
 Gly Pro Gly Arg Val Pro Gly Ala Thr Ala Gly Met Asn Gly Val Asp
 10 15 20 25
 acg tcg ctt ctc tgt gat ttg ttg cag gcc ctg acc ttc ctg acc aga 148
 Thr Ser Leu Leu Cys Asp Leu Leu Gln Ala Leu Thr Phe Leu Thr Arg
 30 35 40
 aat gaa att ctg tgc atc cat gac acc ttc ctg aag ctc tgc cct cct 196
 Asn Glu Ile Leu Cys Ile His Asp Thr Phe Leu Lys Leu Cys Pro Pro
 45 50 55
 ggg aag tac tac aag gag gca acg ctc acc atg gac cag gtc agc tcc 244
 Gly Lys Tyr Tyr Lys Glu Ala Thr Leu Thr Met Asp Gln Val Ser Ser
 60 65 70
 ctg cca gct ctg cgg gtc aac cct ttc aga gac cgt atc tgc aga gtg 292
 Leu Pro Ala Leu Arg Val Asn Pro Phe Arg Asp Arg Ile Cys Arg Val
 75 80 85
 ttc tcc cac aaa ggc atg ttc tcc ttt gag gat gtg ctg ggc atg gca 340
 Phe Ser His Lys Gly Met Phe Ser Phe Glu Asp Val Leu Gly Met Ala
 90 95 100 105
 tct gtg ttc agc gag cag gcc tgc cca agc ctg aag att gag tat gcc 388

Ser	Val	Phe	Ser	Glu	Gln	Ala	Cys	Pro	Ser	Leu	Lys	Ile	Glu	Tyr	Ala	
				110					115					120		
ttt	cgc	atc	tat	gat	ttt	aat	gag	aat	ggc	ttc	att	gat	gag	gag	gat	436
Phe	Arg	Ile	Tyr	Asp	Phe	Asn	Glu	Asn	Gly	Phe	Ile	Asp	Glu	Glu	Asp	
			125					130					135			
ctg	cag	agg	atc	atc	ctg	cga	ctg	ctg	aac	agt	gat	gac	atg	tct	gag	484
Leu	Gln	Arg	Ile	Ile	Leu	Arg	Leu	Leu	Asn	Ser	Asp	Asp	Met	Ser	Glu	
			140				145					150				
gac	ctc	ctg	atg	gac	ctc	acg	aac	cac	gtc	ctg	agt	gag	tcg	gat	ctg	532
Asp	Leu	Leu	Met	Asp	Leu	Thr	Asn	His	Val	Leu	Ser	Glu	Ser	Asp	Leu	
			155			160					165					
gac	aat	gac	aac	atg	ctg	tcc	ttc	tca	gag	ttt	gaa	cat	gca	atg	gcc	580
Asp	Asn	Asp	Asn	Met	Leu	Ser	Phe	Ser	Glu	Phe	Glu	His	Ala	Met	Ala	
			170			175				180				185		
aag	tct	cca	gat	ttc	atg	aac	tcc	ttt	cgg	att	cac	ttc	tg	gga	tgc	628
Lys	Ser	Pro	Asp	Phe	Met	Asn	Ser	Phe	Arg	Ile	His	Phe	Trp	Gly	Cys	
			190					195					200			
tgatgtagcg	gcaaatacct	gacatggcag	cctcgagggga	gaccacagga	atcgaacccc	688										
ctccagcact	ggagggagct	ggtttgaagt	atgactttgt	actggggccca	cactcacctc	748										
tagaatattg	tttattagat	aaaagaaaaa	gcttttcctt	agcccgaaaa	aaaaaaaaaa	808										
t						809										

<210> 56
 <211> 201
 <212> PRT
 <213> Homo sapiens

Met	Leu	Glu	Val	Ser	Asp	Ala	Leu	Gly	Gly	Pro	Gly	Arg	Val	Pro	Gly	
1				5					10					15		
Ala	Thr	Ala	Gly	Met	Asn	Gly	Val	Asp	Thr	Ser	Leu	Leu	Cys	Asp	Leu	
			20					25					30			
Leu	Gln	Ala	Leu	Thr	Phe	Leu	Thr	Arg	Asn	Glu	Ile	Leu	Cys	Ile	His	
			35				40					45				
Asp	Thr	Phe	Leu	Lys	Leu	Cys	Pro	Pro	Gly	Lys	Tyr	Tyr	Lys	Glu	Ala	
			50			55					60					
Thr	Leu	Thr	Met	Asp	Gln	Val	Ser	Ser	Leu	Pro	Ala	Leu	Arg	Val	Asn	
			65			70				75					80	
Pro	Phe	Arg	Asp	Arg	Ile	Cys	Arg	Val	Phe	Ser	His	Lys	Gly	Met	Phe	
			85					90						95		
Ser	Phe	Glu	Asp	Val	Leu	Gly	Met	Ala	Ser	Val	Phe	Ser	Glu	Gln	Ala	
			100					105					110			
Cys	Pro	Ser	Leu	Lys	Ile	Glu	Tyr	Ala	Phe	Arg	Ile	Tyr	Asp	Phe	Asn	
			115				120					125				
Glu	Asn	Gly	Phe	Ile	Asp	Glu	Glu	Asp	Leu	Gln	Arg	Ile	Ile	Leu	Arg	
			130				135				140					
Leu	Leu	Asn	Ser	Asp	Asp	Met	Ser	Glu	Asp	Leu	Leu	Met	Asp	Leu	Thr	
			145			150				155					160	
Asn	His	Val	Leu	Ser	Glu	Ser	Asp	Leu	Asp	Asn	Asp	Asn	Met	Leu	Ser	
			165					170						175		
Phe	Ser	Glu	Phe	Glu	His	Ala	Met	Ala	Lys	Ser	Pro	Asp	Phe	Met	Asn	
			180					185					190			
Ser	Phe	Arg	Ile	His	Phe	Trp	Gly	Cys								
			195					200								

<210> 57
 <211> 1133
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..475

<220>
 <221> CDS
 <222> 476..964

<220>
 <221> 3'UTR
 <222> 965..1133

<220>
 <221> polyA_signal
 <222> 1101..1106

<220>
 <221> polyA_site
 <222> 1118..1133

<400> 57
 gacataatca gagctatgct ggaggagaag agggcagcca tttgctggct ggcttgcagt 60
 gagccaggag gtggcaggac gagttaggag gctggttcag tagctcgggc aagagcaggg 120
 ccccccagga tctgaaggcc tcccaggccc cccaggccca gcgggtccca gaggagagcg 180
 aggaccccaa ggtaactccg gtgagaaggc cgaccaggga tttcaaggcc agccaggctt 240
 tccgggcccc ccgggtcccc ctggattccc aggcaaagtt ggatcacctg gcccacctgg 300
 ccctcaagca gagaagggca gcgaagggat tcgaggccca tcaggcctgc ctggctcccc 360
 tgggccaccg ggacctcctg ggattcaggc ccccgccggt ctggatgggt tggatgggaa 420
 ggatggcaag cctggcttga ggggggaccc tggctctgct ggccccctg gactc atg 478
 Met
 1
 gga cca ccg ggc ttt aag ggg aaa aca gga cat cct ggc ctc cca gga 526
 Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro Gly
 5 10 15
 cct aag ggt gac tgt ggc aaa cca ggt cct cct ggc agc act ggc cgg 574
 Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly Arg
 20 25 30
 cct ggc gca gag ggt gaa cct ggt gcc atg gga ccc cag gga aga ccc 622
 Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg Pro
 35 40 45
 ggt ccc ccg gga cac gtt ggg cca cca ggg cct cca ggc cag cca gga 670
 Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro Gly
 50 55 60 65
 cca gct ggg atc tct gca gtg ggt ctg aaa gga gac cga gga gcc acc 718
 Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala Thr
 70 75 80
 gga gaa agg ggc ctt gca ggc ctc cca ggc cag ccc ggc ccc cca ggt 766
 Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro Gly
 85 90 95
 cct caa ggt cct cca ggc tat ggc aag atg ggt gca aca gga cca atg 814
 Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro Met
 100 105 110
 ggc cag caa ggc atc cct ggc atc cct ggg ccc ccg ggt ccc atg ggc 862
 Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Gly Pro Met Gly
 115 120 125
 cag cca ggc aag gct ggc cac tgt aat ccc tct gac tgc ttt ggg gcc 910
 Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly Ala
 130 135 140 145
 atg ccg atg gag cag cag tac cca ccc atg aaa acc atg aag ggg cct 958
 Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly Pro

```

150
ttt ggc tgaaattccc cacctgcctt tggatgaaag actccgttgg gaataaatgg 1014
Phe Gly
ccaaagctta taggactctg tgacaggttg tgaatgtttt ttttgttggt gttgttggtt 1074
ttaattgctg ttaatatattt ttaaataata aagaacaaaa actaaaaaaaa aaaaaaaaaa 1133

<210> 58
<211> 163
<212> PRT
<213> Homo sapiens

<400> 58
Met Gly Pro Pro Gly Phe Lys Gly Lys Thr Gly His Pro Gly Leu Pro
1 5 10 15
Gly Pro Lys Gly Asp Cys Gly Lys Pro Gly Pro Pro Gly Ser Thr Gly
20 25 30
Arg Pro Gly Ala Glu Gly Glu Pro Gly Ala Met Gly Pro Gln Gly Arg
35 40 45
Pro Gly Pro Pro Gly His Val Gly Pro Pro Gly Pro Pro Gly Gln Pro
50 55 60
Gly Pro Ala Gly Ile Ser Ala Val Gly Leu Lys Gly Asp Arg Gly Ala
65 70 75 80
Thr Gly Glu Arg Gly Leu Ala Gly Leu Pro Gly Gln Pro Gly Pro Pro
85 90 95
Gly Pro Gln Gly Pro Pro Gly Tyr Gly Lys Met Gly Ala Thr Gly Pro
100 105 110
Met Gly Gln Gln Gly Ile Pro Gly Ile Pro Gly Pro Pro Gly Pro Met
115 120 125
Gly Gln Pro Gly Lys Ala Gly His Cys Asn Pro Ser Asp Cys Phe Gly
130 135 140
Ala Met Pro Met Glu Gln Gln Tyr Pro Pro Met Lys Thr Met Lys Gly
145 150 155 160
Pro Phe Gly

<210> 59
<211> 838
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..78

<220>
<221> CDS
<222> 79..642

<220>
<221> 3'UTR
<222> 643..838

<220>
<221> polyA_signal
<222> 799..804

<220>
<221> polyA_site
<222> 823..838

<400> 59

```

```

aaagactgcg tgcagaaggt gactgtctca gtggagctgg gtcattctcag gccttggctc 60
cttgaacttt tggccgcc atg tgc ttc ccg aag gtc ctc tct gat gac atg 111
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met
1 5 10
aag aag ctg aag gcc cga atg cac cag gcc ata gaa aga ttt tat gat 159
Lys Lys Leu Lys Ala Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp
15 20 25
aaa atg caa aat gca gaa tca gga cgt gga cag gtg atg tcg agc ctg 207
Lys Met Gln Asn Ala Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu
30 35 40
gca gag ctg gag gac gac ttc aaa gag ggc tac ctg gag aca gtg gcg 255
Ala Glu Leu Glu Asp Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala
45 50 55
gct tat tat gag gag cag cac cca gag ctc act cct cta ctt gaa aaa 303
Ala Tyr Tyr Glu Glu Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys
60 65 70 75
gaa aga gat gga tta cgg tgc cga ggc aac aga tcc cct gtc ccg gat 351
Glu Arg Asp Gly Leu Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp
80 85 90
gtt gag gat ccc gca acc gag gag cct ggg gag agc ttt tgt gac aag 399
Val Glu Asp Pro Ala Thr Glu Glu Pro Gly Glu Ser Phe Cys Asp Lys
95 100 105
gtc atg aga tgg ttc cag gcc atg ctg cag cgg ctg cag acc tgg tgg 447
Val Met Arg Trp Phe Gln Ala Met Leu Gln Arg Leu Gln Thr Trp Trp
110 115 120
cac ggg gtt ctg gcc tgg gtg aag gag aag gtg gtg gcc ctg gtc cat 495
His Gly Val Leu Ala Trp Val Lys Glu Lys Val Val Ala Leu Val His
125 130 135
gca gtg cag gcc ctc tgg aaa cag ttc cag agt ttc tgc tgc tct ctg 543
Ala Val Gln Ala Leu Trp Lys Gln Phe Gln Ser Phe Cys Cys Ser Leu
140 145 150 155
tca gag ctc ttc atg tcc tct ttc cag tcc tac gga gcc cca cgg ggg 591
Ser Glu Leu Phe Met Ser Ser Phe Gln Ser Tyr Gly Ala Pro Arg Gly
160 165 170
gac aag gag gag ctg aca ccc cag aag tgc tct gaa ccc caa tcc tca 639
Asp Lys Glu Glu Leu Thr Pro Gln Lys Cys Ser Glu Pro Gln Ser Ser
175 180 185
aaa tgaagatact gacaccacct ttgccctccc cgtcaccgcg caccaccct 692
Lys
gacccctccc tcagctgtcc tgtgccccgc cctctcccg acactcagtc cccctgctg 752
gcgttcctgc cgcagctctg acctggtgct gtcgccctgg catcttaata aamcctgctt 812
atacttccct aaaaaaaaaa aaaaaa 838

```

<210> 60
 <211> 188
 <212> PRT
 <213> Homo sapiens

```

<400> 60
Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
1 5 10 15
Arg Met His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala
20 25 30
Glu Ser Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp
35 40 45
Asp Phe Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu
50 55 60
Gln His Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu
65 70 75 80
Arg Cys Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala

```


				85					90					95			
Thr	Glu	Glu	Pro	Gly	Glu	Ser	Phe	Cys	Asp	Lys	Val	Met	Arg	Trp	Phe		
			100					105					110				
Gln	Ala	Met	Leu	Gln	Arg	Leu	Gln	Thr	Trp	Trp	His	Gly	Val	Leu	Ala		
		115					120					125					
Trp	Val	Lys	Glu	Lys	Val	Val	Ala	Leu	Val	His	Ala	Val	Gln	Ala	Leu		
	130						135					140					
Trp	Lys	Gln	Phe	Gln	Ser	Phe	Cys	Cys	Ser	Leu	Ser	Glu	Leu	Phe	Met		
145					150					155					160		
Ser	Ser	Phe	Gln	Ser	Tyr	Gly	Ala	Pro	Arg	Gly	Asp	Lys	Glu	Glu	Leu		
				165					170					175			
Thr	Pro	Gln	Lys	Cys	Ser	Glu	Pro	Gln	Ser	Ser	Lys						
			180					185									

<210> 61
 <211> 862
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..158

<220>
 <221> CDS
 <222> 159..764

<220>
 <221> 3'UTR
 <222> 765..862

<400> 61
 attttttttt ttggcagcgc tgcagccaag ttggggaggg ttctctggac agaggtcctt 60
 tggctgctgc cttaagacgt gcagcctggg ccgtggctgt cactgcgttc ggaccagac 120
 ccgctgcagg cagcagcagc ccccgcccgc gcagcagc atg gag ctc tgg ggg gcc 176
 Met Glu Leu Trp Gly Ala
 -20 -15
 tac ctc ctc ctc tgc ctc ttc tcc ctc ctg acc cag gtc acc acc gag 224
 Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu Thr Gln Val Thr Thr Glu
 -10 -5 1
 cca cca acc cag aag ccc aag aag att gta aat gcc aag aaa gat gtt 272
 Pro Pro Thr Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp Val
 5 10 15
 gtg aac aca aag atg ttt gag gag ctc aag agc cgt ctg gac acc ctg 320
 Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr Leu
 20 25 30
 gcc cag gag gtg gcc ctg ctg aag gag cag cag gcc ctg cag acg gtc 368
 Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr Val
 35 40 45 50
 tgc ctg aag ggg acc aag gtg cac atg aaa tgc ttt ctg gcc ttc acc 416
 Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe Thr
 55 60 65
 cag acg aag acc ttc cac gag tcc agc gag gac tgc atc tcg cgc ggg 464
 Gln Thr Lys Thr Phe His Glu Ser Ser Glu Asp Cys Ile Ser Arg Gly
 70 75 80
 ggc acc ctg agc acc cct cag act ggc tcg gag aac gac gcc ctg tat 512
 Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu Tyr
 85 90 95
 gag tac ctg cgc cag agc gtg ggc aac gag gcc gag atc tgg ctg ggc 560
 Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu Gly

```

      100              105              110
ctc aac gac atg gcg gcc gag ggc acc tgg gtg gac atg acc ggc gcc 608
Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly Ala
115              120              125              130
cgc atc gcc tac aag aac tgg gag act gag atc acc gcg caa ccc gat 656
Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro Asp
      135              140              145
ggc ggc aag acc gag aac tgc gcg gtc ctg tca ggc gcg gcc aac ggc 704
Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn Gly
      150              155              160
aag tgg ttc gac aag cgc tgc cgc gat cag ctg ccc tac atc tgc cag 752
Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys Gln
      165              170              175
ttc ggg atc gtg tagccggcgg ggcggggggcc gtggggggggcc tggaggaggg 804
Phe Gly Ile Val
      180
caggagccgc gggaggcccg gaggaggggtg gggaccttgc agcccccatc ctctccgt 862

<210> 62
<211> 202
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..21

<400> 62
Met Glu Leu Trp Gly Ala Tyr Leu Leu Leu Cys Leu Phe Ser Leu Leu
-20 -15 -10
Thr Gln Val Thr Thr Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val
-5 1 5 10
Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
15 20 25
Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
30 35 40
Gln Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys
45 50 55
Cys Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ser Ser Glu
60 65 70 75
Asp Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser
80 85 90
Glu Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu
95 100 105
Ala Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp
110 115 120
Val Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu
125 130 135
Ile Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu
140 145 150 155
Ser Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln
160 165 170
Leu Pro Tyr Ile Cys Gln Phe Gly Ile Val
175 180

<210> 63
<211> 618
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..194

<220>
<221> CDS
<222> 195..587

<220>
<221> 3'UTR
<222> 588..618

<220>
<221> polyA_signal
<222> 578..583

<220>
<221> polyA_site
<222> 604..618

<400> 63
atttgcttag gtctgatcaa tctgctccac acaatttctc agtgatcctc tgcattctctg 60
cctacaaggg cctccctgac acccaagttc atattgctca gaaacagtga acttgagttt 120
ttcgttttac cttgatctct ctctgacaaa gaaatccaga tgatgcgaga cctgatgaag 180
acaatacatg gaaa atg aca gtc ttg gaa ata act ttg gct gtc atc ctg 230
                Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu
                -20                                -15                                -10
act cta ctg gga ctt gcc atc ctg gct att ttg tta aca aga tgg gca 278
Thr Leu Leu Gly Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala
                -5                                1                                5
cga cgt aag caa agt gaa atg cat atc tcc aga tac agt tca gaa caa 326
Arg Arg Lys Gln Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln
                10                                15                                20
agt gct aga ctt ctg gac tat gag gat ggt aga gga tcc cga cat gca 374
Ser Ala Arg Leu Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala
                25                                30                                35
tat tca aca caa agt gag aga tcc aaa aga gat tac aca cca tca acc 422
Tyr Ser Thr Gln Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr
40                                45                                50                                55
aac tct cta gca ctg tct cga tca agt att gct tta cct caa gga tcc 470
Asn Ser Leu Ala Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser
                60                                65                                70
atg agt agt ata aaa tgt tta caa aca act gaa gaa ctt cct tcc aga 518
Met Ser Ser Ile Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg
                75                                80                                85
act gca gga gcc atg agt aag ttc ttt ttc tgc cct tta att ctg atg 566
Thr Ala Gly Ala Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met
                90                                95                                100
tgc ttt gct tta cta aac tgt tagaatatgt aagacgaaaa aaaaaaaaaa a 618
Cys Phe Ala Leu Leu Asn Cys
                105                                110

<210> 64
<211> 131
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..22

```

<400> 64
Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
-20 -15 -10
Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
-5 1 5 10
Ser Glu Met His Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
15 20 25
Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
30 35 40
Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
45 50 55
Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
60 65 70
Lys Cys Leu Gln Thr Thr Glu Glu Leu Pro Ser Arg Thr Ala Gly Ala
75 80 85 90
Met Ser Lys Phe Phe Phe Cys Pro Leu Ile Leu Met Cys Phe Ala Leu
95 100 105
Leu Asn Cys

<210> 65
<211> 836
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..176

<220>
<221> CDS
<222> 177..767

<220>
<221> 3'UTR
<222> 768..836

<220>
<221> polyA_signal
<222> 814..819

<220>
<221> polyA_site
<222> 822..836

<400> 65
aatctgctcc acgcaatttc tcagtgatcc tctgcatctc tgcctacaag ggcctccctg 60
acacccaagt tcatattgct cagaaacagt gaacttgagt ttttcatttt accttgatct 120
ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaataca tggaaa atg 179
Met
aca gtc ttg gaa ata act ttg gct gtc atc ctg act cta ctg gga ctt 227
Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
-20 -15 -10 -5
gcc atc ctg gct att ttg tta aca aga tgg gca cga cgt aag caa agt 275
Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln Ser
1 5 10
gaa atg tat atc tcc aga tac agt tca gaa caa agt gct aga ctt ctg 323
Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu
15 20 25
gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt 371

Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser
 30 35 40
 gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg 419
 Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu
 45 50 55 60
 tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa 467
 Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys
 65 70 75
 tgt tta caa aca act gaa gaa cct cct tcc aga act gca gga gcc atg 515
 Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
 80 85 90
 atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc 563
 Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu
 95 100 105
 tct caa aaa acc att gtg caa act cta gga cct att gta caa tat cct 611
 Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro
 110 115 120
 gga tcc aat ggg agg ata aac ata agc cag ctc acc tca gag gat ctc 659
 Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp Leu
 125 130 135 140
 act ggg gct aaa gga agg gtc aca tct ggt cca cag ttc cct aat agc 707
 Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser
 145 150 155
 cac cat gtg cca gag aat cta cat gga tac atg aat tcc ctt tcc ctt 755
 His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu
 160 165 170
 ttc tcc cct gct tgactccctc tcccttatgt gtaaacaatt taaaaatatg 807
 Phe Ser Pro Ala
 175
 atagtgtata aatgaaaaaa aaaaaaaaaa 836

 <210> 66
 <211> 197
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> SIGNAL
 <222> 1..22

 <400> 66
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
 -20 -15 -10
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
 -5 1 5 10
 Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
 15 20 25
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
 30 35 40
 Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
 45 50 55
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
 60 65 70
 Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala
 75 80 85 90
 Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys
 95 100 105
 Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr
 110 115 120
 Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp

125 130 135
 Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn
 140 145 150
 Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser
 155 160 165 170
 Leu Phe Ser Pro Ala
 175

<210> 67
 <211> 789
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..62

<220>
 <221> CDS
 <222> 63..572

<220>
 <221> 3'UTR
 <222> 573..789

<220>
 <221> polyA_signal
 <222> 750..755

<220>
 <221> polyA_site
 <222> 774..789

<400> 67
 atatgtcatc aggcccccgc cctgggaggt gtgctgccag agattttgcc tcttcaaggt 60
 ga atg cgg ctt caa ggg gct atc ttt gtg ctc ctg ccc cac ctg ggg 107
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
 1 5 10 15
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
 20 25 30
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt cgc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491

Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
 145 150 155
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 160 165 170
 gagggaggac gcccaggggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggtt 652
 caccccaatg ggaccaccct cctgggtccc ctgggtgccgt ttttccttag aaatçagaga 712
 aatgggaaag ggggggaaac tgattttaca cttaaataat aaaatcctat tagtaactcc 772
 gaaaaaaaa aaaaaaa 789

<210> 68
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly Pro
 1 5 10 15
 Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys Glu
 20 25 30
 Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu Leu
 35 40 45
 Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu Val
 50 55 60
 Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro Leu
 65 70 75 80
 Arg Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val Leu
 85 90 95
 Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu Leu
 100 105 110
 Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile Asn
 115 120 125
 Lys Leu Ala Ala Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr Val
 130 135 140
 Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro Val
 145 150 155 160
 His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 165 170

<210> 69
 <211> 2556
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..66

<220>
 <221> CDS
 <222> 67..2427

<220>
 <221> 3'UTR
 <222> 2428..2556

<220>

<221> polyA_signal

<222> 2522..2527

<220>

<221> polyA_site

<222> 2541..2556

<400> 69

```
gtccccgcgt ccctggcaat tcccgacttc ccaacggctt cctgctggca gccccgaagc 60
cgcacc atg ttc cgc ctc tgg ttg ctg ctg gcc ggg ctc tgc ggc ctc 108
      Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu
      -15 -10 -5
ctg gcg tca aga ccc ggt ttt caa aat tca ctt cta cag atc gta att 156
Leu Ala Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile
      1 5 10 15
cca gag aaa atc caa aca aat aca aat gac agt tca gaa ata gaa tat 204
Pro Glu Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr
      20 25 30
gaa caa ata tcc tat att att cca ata gat gag aaa ctg tac act gtg 252
Glu Gln Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val
      35 40 45
cac ctt aaa caa aga tat ttt tta aca gat aat ttt atg atc tat ttg 300
His Leu Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu
      50 55 60
tac aat caa gga tct atg aat act tat tct tca gat att cag act caa 348
Tyr Asn Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln
      65 70 75
tgc tac tat caa gga aat att gaa gaa tat cca gat tcc atg gtc aca 396
Cys Tyr Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr
      80 85 90 95
ctc agc acg tgc tct gga cta aga gga ata ctg caa ttt gaa aat gtt 444
Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val
      100 105 110
tct tat gga att gag cct ctg gaa tct gca gtt gaa ttt cag cat gtt 492
Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val
      115 120 125
ctt cac aaa tta aag aat gaa gac aat gat att gca att ttt att gac 540
Leu His Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp
      130 135 140
aga agc ctg aaa gaa caa cca atg gat gac aac att ttt ata agt gaa 588
Arg Ser Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu
      145 150 155
aaa tca gaa cca gct gtt cca gat tta ttt cct ctt tat cta gaa atg 636
Lys Ser Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met
      160 165 170 175
cat att gtg gtg gac aaa act ttg tat gat tac tgg ggc tct gat agc 684
His Ile Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser
      180 185 190
atg ata gta aca aat aaa gtc atc gaa att gtt ggc ctt gca aat tca 732
Met Ile Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser
      195 200 205
atg ttc acc caa ttt aaa gtt act att gtg ctg tca tca ttg gag tta 780
Met Phe Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu
      210 215 220
tgg tca gat gaa aat aag att tct aca gtt ggt gag gca gat gaa tta 828
Trp Ser Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu
      225 230 235
ttg caa aaa ttt tta gaa tgg aaa caa tct tat ctt aac cta agg cct 876
Leu Gln Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro
      240 245 250 255
```


cat gat att gca tat cta cta att tat atg gat tat cct cgt tat ttg	924
His Asp Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu	
260 265 270	
gga gca gtg ttt cct gga aca atg tgt att act cgt tat tct gca gga	972
Gly Ala Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly	
275 280 285	
gtc gca ttg tac ccc aag gag ata act ctg gag gca ttt gca gtt att	1020
Val Ala Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile	
290 295 300	
gtc acc cag atg ctg gca ctc agt ctg gga ata tca tat gac gac cca	1068
Val Thr Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro	
305 310 315	
aag aaa tgt caa tgt tca gaa tcc acc tgt ata atg aat cca gaa gtt	1116
Lys Lys Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val	
320 325 330 335	
gtg caa tcc aat ggt gtg aag act ttt agc agt tgc agt ttg agg agc	1164
Val Gln Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser	
340 345 350	
ttt caa aat ttc att tca aat gtg ggt gtc aaa tgt ctt cag aat aag	1212
Phe Gln Asn Phe Ile Ser Asn Val Gly Val Lys Cys Leu Gln Asn Lys	
355 360 365	
cca caa atg caa aaa aaa tct ccg aaa cca gtc tgt ggc aat ggc aga	1260
Pro Gln Met Gln Lys Lys Ser Pro Lys Pro Val Cys Gly Asn Gly Arg	
370 375 380	
ttg gag gga aat gaa atc tgt gat tgt ggt act gag gct caa tgt gga	1308
Leu Glu Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala Gln Cys Gly	
385 390 395	
cct gca agc tgt tgt gat ttt cga act tgt gta ctg aaa gac gga gca	1356
Pro Ala Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala	
400 405 410 415	
aaa tgt tat aaa gga ctg tgc tgc aaa gac tgt caa att tta caa tca	1404
Lys Cys Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser	
420 425 430	
ggc gtt gaa tgt agg ccg aaa gca cat cct gaa tgt gac atc gct gaa	1452
Gly Val Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu	
435 440 445	
aat tgt aat gga agc tca cca gaa tgt ggt cct gac ata act tta atc	1500
Asn Cys Asn Gly Ser Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile	
450 455 460	
aat gga ctt tca tgc aaa aat aat aag ttt att tgt tat gac gga gac	1548
Asn Gly Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp	
465 470 475	
tgc cat gat ctc gat gca cgt tgt gag agt gta ttt gga aaa ggt tca	1596
Cys His Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser	
480 485 490 495	
aga aat gct cca ttt gcc tgc tat gaa gaa ata caa tct caa tca gac	1644
Arg Asn Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp	
500 505 510	
aga ttt ggg aac tgt ggt agg gat aga aat aac aaa tat gtg ttc tgt	1692
Arg Phe Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys	
515 520 525	
gga tgg agg aat ctt ata tgt gga aga tta gtt tgt acc tac cct act	1740
Gly Trp Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr	
530 535 540	
cga aag cct ttc cat caa gaa aat ggt gat gtg att tat gct ttc gta	1788
Arg Lys Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val	
545 550 555	
cga gat tct gta tgc ata acc gta gac tac aaa ttg cct cga aca gtt	1836
Arg Asp Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val	
560 565 570 575	

```

cca gat cca ctg gct gtc aaa aat ggc tct cag tgt gat att ggg agg 1884
Pro Asp Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg
580 585 590
gtt tgt gta aat cgt gaa tgt gta gaa tca agg ata att aag gct tca 1932
Val Cys Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser
595 600 605
gca cat gtt tgt tca caa cag tgt tct gga cat gga gtg tgt gat tcc 1980
Ala His Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser
610 615 620
aga aac aag tgc cat tgt tgc cca ggc tat aag cct cca aac tgc caa 2028
Arg Asn Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln
625 630 635
ata cgt tcc aaa gga ttt tcc ata ttt cct gag gaa gat atg ggt tca 2076
Ile Arg Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser
640 645 650 655
atc atg gaa aga gca tct ggg aag act gaa aac acc tgg ctt cta ggt 2124
Ile Met Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly
660 665 670
ttc ctc att gct ctt cct att ctc att gta aca acc gca ata gtt ttg 2172
Phe Leu Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu
675 680 685
gca agg aaa cag ttg aaa aac tgg ttc gcc aag gaa gag gaa ttc cca 2220
Ala Arg Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro
690 695 700
agt agc gaa tct aaa tcg gaa ggt agc aca cag aca tat gcc agc caa 2268
Ser Ser Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln
705 710 715
tcc agc tca gaa ggc agc act cag aca tat gcc ggc caa acc aga tca 2316
Ser Ser Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser
720 725 730 735
gaa agc agc agt caa gct gat act agc aaa tcc aaa tca gaa gat agt 2364
Glu Ser Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser
740 745 750
gct gaa gca tat act agc aga tcc aaa tca cag gac agt acc caa aca 2412
Ala Glu Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr
755 760 765
caa agc agt agt aac tagtgattcc ttcagaaggc aacggataac atcgagagtc 2467
Gln Ser Ser Ser Asn
770
tcgctaagaa atgaaaattc tgtctttcct tccgtgggtca cagctgaaag aaacaataaa 2527
ttgagtgtgg accaaaaaaa aaaaaaaat 2556

```

<210> 70
 <211> 787
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..16

<400> 70
 Met Phe Arg Leu Trp Leu Leu Leu Ala Gly Leu Cys Gly Leu Leu Ala
 -15 -10 -5
 Ser Arg Pro Gly Phe Gln Asn Ser Leu Leu Gln Ile Val Ile Pro Glu
 1 5 10 15
 Lys Ile Gln Thr Asn Thr Asn Asp Ser Ser Glu Ile Glu Tyr Glu Gln
 20 25 30
 Ile Ser Tyr Ile Ile Pro Ile Asp Glu Lys Leu Tyr Thr Val His Leu
 35 40 45

Lys Gln Arg Tyr Phe Leu Thr Asp Asn Phe Met Ile Tyr Leu Tyr Asn
 50 55 60
 Gln Gly Ser Met Asn Thr Tyr Ser Ser Asp Ile Gln Thr Gln Cys Tyr
 65 70 75 80
 Tyr Gln Gly Asn Ile Glu Glu Tyr Pro Asp Ser Met Val Thr Leu Ser
 85 90 95
 Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Phe Glu Asn Val Ser Tyr
 100 105 110
 Gly Ile Glu Pro Leu Glu Ser Ala Val Glu Phe Gln His Val Leu His
 115 120 125
 Lys Leu Lys Asn Glu Asp Asn Asp Ile Ala Ile Phe Ile Asp Arg Ser
 130 135 140
 Leu Lys Glu Gln Pro Met Asp Asp Asn Ile Phe Ile Ser Glu Lys Ser
 145 150 155 160
 Glu Pro Ala Val Pro Asp Leu Phe Pro Leu Tyr Leu Glu Met His Ile
 165 170 175
 Val Val Asp Lys Thr Leu Tyr Asp Tyr Trp Gly Ser Asp Ser Met Ile
 180 185 190
 Val Thr Asn Lys Val Ile Glu Ile Val Gly Leu Ala Asn Ser Met Phe
 195 200 205
 Thr Gln Phe Lys Val Thr Ile Val Leu Ser Ser Leu Glu Leu Trp Ser
 210 215 220
 Asp Glu Asn Lys Ile Ser Thr Val Gly Glu Ala Asp Glu Leu Leu Gln
 225 230 235 240
 Lys Phe Leu Glu Trp Lys Gln Ser Tyr Leu Asn Leu Arg Pro His Asp
 245 250 255
 Ile Ala Tyr Leu Leu Ile Tyr Met Asp Tyr Pro Arg Tyr Leu Gly Ala
 260 265 270
 Val Phe Pro Gly Thr Met Cys Ile Thr Arg Tyr Ser Ala Gly Val Ala
 275 280 285
 Leu Tyr Pro Lys Glu Ile Thr Leu Glu Ala Phe Ala Val Ile Val Thr
 290 295 300
 Gln Met Leu Ala Leu Ser Leu Gly Ile Ser Tyr Asp Asp Pro Lys Lys
 305 310 315 320
 Cys Gln Cys Ser Glu Ser Thr Cys Ile Met Asn Pro Glu Val Val Gln
 325 330 335
 Ser Asn Gly Val Lys Thr Phe Ser Ser Cys Ser Leu Arg Ser Phe Gln
 340 345 350
 Asn Phe Ile Ser Asn Val Gly Val Lys Cys Leu Gln Asn Lys Pro Gln
 355 360 365
 Met Gln Lys Lys Ser Pro Lys Pro Val Cys Gly Asn Gly Arg Leu Glu
 370 375 380
 Gly Asn Glu Ile Cys Asp Cys Gly Thr Glu Ala Gln Cys Gly Pro Ala
 385 390 395 400
 Ser Cys Cys Asp Phe Arg Thr Cys Val Leu Lys Asp Gly Ala Lys Cys
 405 410 415
 Tyr Lys Gly Leu Cys Cys Lys Asp Cys Gln Ile Leu Gln Ser Gly Val
 420 425 430
 Glu Cys Arg Pro Lys Ala His Pro Glu Cys Asp Ile Ala Glu Asn Cys
 435 440 445
 Asn Gly Ser Ser Pro Glu Cys Gly Pro Asp Ile Thr Leu Ile Asn Gly
 450 455 460
 Leu Ser Cys Lys Asn Asn Lys Phe Ile Cys Tyr Asp Gly Asp Cys His
 465 470 475 480
 Asp Leu Asp Ala Arg Cys Glu Ser Val Phe Gly Lys Gly Ser Arg Asn
 485 490 495
 Ala Pro Phe Ala Cys Tyr Glu Glu Ile Gln Ser Gln Ser Asp Arg Phe
 500 505 510
 Gly Asn Cys Gly Arg Asp Arg Asn Asn Lys Tyr Val Phe Cys Gly Trp
 515 520 525

Arg Asn Leu Ile Cys Gly Arg Leu Val Cys Thr Tyr Pro Thr Arg Lys
 530 535 540
 Pro Phe His Gln Glu Asn Gly Asp Val Ile Tyr Ala Phe Val Arg Asp
 545 550 555 560
 Ser Val Cys Ile Thr Val Asp Tyr Lys Leu Pro Arg Thr Val Pro Asp
 565 570 575
 Pro Leu Ala Val Lys Asn Gly Ser Gln Cys Asp Ile Gly Arg Val Cys
 580 585 590
 Val Asn Arg Glu Cys Val Glu Ser Arg Ile Ile Lys Ala Ser Ala His
 595 600 605
 Val Cys Ser Gln Gln Cys Ser Gly His Gly Val Cys Asp Ser Arg Asn
 610 615 620
 Lys Cys His Cys Ser Pro Gly Tyr Lys Pro Pro Asn Cys Gln Ile Arg
 625 630 635 640
 Ser Lys Gly Phe Ser Ile Phe Pro Glu Glu Asp Met Gly Ser Ile Met
 645 650 655
 Glu Arg Ala Ser Gly Lys Thr Glu Asn Thr Trp Leu Leu Gly Phe Leu
 660 665 670
 Ile Ala Leu Pro Ile Leu Ile Val Thr Thr Ala Ile Val Leu Ala Arg
 675 680 685
 Lys Gln Leu Lys Asn Trp Phe Ala Lys Glu Glu Glu Phe Pro Ser Ser
 690 695 700
 Glu Ser Lys Ser Glu Gly Ser Thr Gln Thr Tyr Ala Ser Gln Ser Ser
 705 710 715 720
 Ser Glu Gly Ser Thr Gln Thr Tyr Ala Gly Gln Thr Arg Ser Glu Ser
 725 730 735
 Ser Ser Gln Ala Asp Thr Ser Lys Ser Lys Ser Glu Asp Ser Ala Glu
 740 745 750
 Ala Tyr Thr Ser Arg Ser Lys Ser Gln Asp Ser Thr Gln Thr Gln Ser
 755 760 765
 Ser Ser Asn
 770

<210> 71
 <211> 1603
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..7

<220>
 <221> CDS
 <222> 8..763

<220>
 <221> 3'UTR
 <222> 764..1603

<220>
 <221> polyA_signal
 <222> 1562..1567

<220>
 <221> polyA_site
 <222> 1588..1603

<220>
 <221> UNSURE

<222> 157

<223> Xaa = Ala,Gly

<400> 71

```
gagaagg atg ggg ccg cat cta cac ctg tgc ctg tgt gtg cct gac ctg      49
      Met Gly Pro His Leu His Leu Cys Leu Cys Val Pro Asp Leu
      -15                                -10                                -5
cgg tca ctc cgt gtc tgt gtg tcc ctc tgg tct gtc cac cac agg cca      97
Arg Ser Leu Arg Val Cys Val Ser Leu Trp Ser Val His His Arg Pro
      1                                5                                10
cac gag tcc ctg gcc cgg gag gag gcc ctc act gca ctt ggg aag ctc      145
His Glu Ser Leu Ala Arg Glu Glu Ala Leu Thr Ala Leu Gly Lys Leu
      15                                20                                25                                30
ctg tac ctc tta gat ggg atg ctg gat ggg cag gtg aac agt ggt ata      193
Leu Tyr Leu Leu Asp Gly Met Leu Asp Gly Gln Val Asn Ser Gly Ile
      35                                40                                45
gca gcc act cca gcc tct gct gca gca gcc acc ctg gat gtg gct gtt      241
Ala Ala Thr Pro Ala Ser Ala Ala Ala Thr Leu Asp Val Ala Val
      50                                55                                60
cgg aga ggc ctg tcc cac gca gcc cag agg ctg ctg tgc gtg gcc ctg      289
Arg Arg Gly Leu Ser His Ala Ala Gln Arg Leu Leu Cys Val Ala Leu
      65                                70                                75
gga cag ctg gac cgg cct cca gac ctc gcc cat gac ggg agg agt ctg      337
Gly Gln Leu Asp Arg Pro Pro Asp Leu Ala His Asp Gly Arg Ser Leu
      80                                85                                90
tgg ctg aac atc agg ggc aag gag gcg gct gcc cta tcc atg ttc cat      385
Trp Leu Asn Ile Arg Gly Lys Glu Ala Ala Leu Ser Met Phe His
      95                                100                                105                                110
gtc tcc acg cca ctg cca gtg atg acc ggt ggt ttc ctg agc tgc atc      433
Val Ser Thr Pro Leu Pro Val Met Thr Gly Gly Phe Leu Ser Cys Ile
      115                                120                                125
ttg ggc ttg gtg ctg ccc ctg gcc tat ggc ttc cag cct gac ctg gtg      481
Leu Gly Leu Val Leu Pro Leu Ala Tyr Gly Phe Gln Pro Asp Leu Val
      130                                135                                140
ctg gtg gcg ctg ggg cct ggc cat ggc ctg cag ggc ccc cac gst gca      529
Leu Val Ala Leu Gly Pro Gly His Gly Leu Gln Gly Pro His Xaa Ala
      145                                150                                155
ctc ctg gct gca atg ctt cgg ggg ctg gca ggg ggc cga gtc ctg gcc      577
Leu Leu Ala Ala Met Leu Arg Gly Leu Ala Gly Gly Arg Val Leu Ala
      160                                165                                170
ctc ctg gag gag aac tcc aca ccc cag cta gca ggg atc ctg gcc cgg      625
Leu Leu Glu Glu Asn Ser Thr Pro Gln Leu Ala Gly Ile Leu Ala Arg
      175                                180                                185                                190
gtg ctg aat gga gag gca cct cct agc cta ggc cct tcc tct gtg gcc      673
Val Leu Asn Gly Glu Ala Pro Pro Ser Leu Gly Pro Ser Ser Val Ala
      195                                200                                205
tcc cca gag gac gtc cag gcc ctg atg tac ctg aga ggg cag ctg gag      721
Ser Pro Glu Asp Val Gln Ala Leu Met Tyr Leu Arg Gly Gln Leu Glu
      210                                215                                220
cct cag tgg aag atg ttg cag tgc cat cct cac ctg gtg gct      763
Pro Gln Trp Lys Met Leu Gln Cys His Pro His Leu Val Ala
      225                                230                                235
tgaaatcggc caaggtggga gcatttacac cgcagaaatg acaccgcacg ccagcgcgcc 823
gcggccgcga tccggacccc aagccacagg ctccctcgac tctggggcac ggaaccccg 883
ccactcccaa tccccgcgcc ccgccctctc ccaccctgac ttcccccgct ccaccctca 943
cctcacctcg cccccgcccc acccatcgcg ccccgggcggc tggtattggt cggctgggct 1003
cggtcggggcg ctgtctccct cggctctgcg ggtgtcagtt cgtccggctt cctcacagcc 1063
cctcactccc ggcggtgac agcagcagcg gcggcgggcg gcggcgctg gcgtttcgag 1123
gctgagcggc accggggttg gggcgcgag gaggagcagc agcgggagga ggagccgtgt 1183
gccctggcac tgagcggccg cggccatggc gtacgcctat ctcttcaagt acatcataat 1243
```


<220>
 <221> 5'UTR
 <222> 1..8

<220>
 <221> CDS
 <222> 9..395

<220>
 <221> 3'UTR
 <222> 396..879

<220>
 <221> polyA_site
 <222> 864..879

<400> 73

```

aggccaac atg gcc gtg ctg ctg ctg ctg ctc cgt gcc ctc cgc cgg ggt 50
      Met Ala Val Leu Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly
      -15              -10              -5
cca ggc ccg ggt cct cgg ccg ctg tgg ggc cca ggc ccg gcc tgg agt 98
Pro Gly Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser
      1              5              10              15
cca ggg ttc ccc gcc agg ccc ggg agg ggg cgg ccg tac atg gcc agc 146
Pro Gly Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser
      20              25              30
agg cct ccg ggg gac ctc gcc gag gct gga ggc cga gct ctg cag agc 194
Arg Pro Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser
      35              40              45
tta caa ttg aga ctg cta acc cct acc ttt gaa ggg atc aac gga ttg 242
Leu Gln Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu
      50              55              60
ttg ttg aaa caa cat tta gtt cag aat cca gtc aga ctc tgg caa ctt 290
Leu Leu Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu
      65              70              75
tta ggt ggt act ttc tat ttt aac acc tca agg ttg aag cag aag aat 338
Leu Gly Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn
      80              85              90              95
aag gag aag gat aag tcg aag ggg aag gcg cct gaa gag gac gaa ggt 386
Lys Glu Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly
      100              105              110
ata ttc atc tgatgttctt cagtcagtag ctgcctctgg atgtctttac 435
Ile Phe Ile
rtttctgttt wccttttagc aaggtgaaac cagtctggam aatggggaga tgggcccgggt 495
gcagtggctc acacttgtaa tcgaaacgct ttgggaggcc caggtggaag gatcacttga 555
ggcctatacc acatagctag accctgtctc actgcaaatt aaaaggctgg gcgtggtggc 615
tcacacctgt aatcccagca ctttgggagg ctgaggcagg cggatcacct gcacctggc 675
caacatggtg aaaccccgct tttactaaaa atagaaaatt agccgggctg gatggcacac 735
gcctgtaatc ccagctactc gggaggctga ggcaggagaa ttgcttgaac ctgggagggtg 795
gaggttgctg tgagtggaga tcatgccatt gcactccagc ctgagcaaca agagcaaaac 855
tccatcccaa aaaaaaaaaa aaaa 879

```

<210> 74
 <211> 129
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..16

<400> 74
Met Ala Val Leu Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly Pro Gly
-15 -10 -5
Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser Pro Gly
1 5 10 15
Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala Ser Arg Pro
20 25 30
Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu Gln Ser Leu Gln
35 40 45
Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile Asn Gly Leu Leu Leu
50 55 60
Lys Gln His Leu Val Gln Asn Pro Val Arg Leu Trp Gln Leu Leu Gly
65 70 75 80
Gly Thr Phe Tyr Phe Asn Thr Ser Arg Leu Lys Gln Lys Asn Lys Glu
85 90 95
Lys Asp Lys Ser Lys Gly Lys Ala Pro Glu Glu Asp Glu Gly Ile Phe
100 105 110
Ile

<210> 75
<211> 1634
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..87

<220>
<221> CDS
<222> 88..1269

<220>
<221> 3'UTR
<222> 1270..1634

<220>
<221> polyA_signal
<222> 1594..1599

<220>
<221> polyA_site
<222> 1619..1634

<400> 75
aaagttcctc agcccttggc tcctgcccag tgtttagggg gttggcggag acaaagggga 60
agagtcacgc cctgtcgggg ctaggat atg atg ggt gtg ttt gta gtt gct gct 114
Met Met Gly Val Phe Val Val Ala Ala
1 5
aag cga acg ccc ttt gga gct tac gga ggc ctt ctg aaa gac ttc act 162
Lys Arg Thr Pro Phe Gly Ala Tyr Gly Gly Leu Leu Lys Asp Phe Thr
10 15 20 25
gct act gac ttg tct gaa ttt gct gcc aag gct gcc ttg tct gct ggc 210
Ala Thr Asp Leu Ser Glu Phe Ala Ala Lys Ala Ala Leu Ser Ala Gly
30 35 40
aaa gtc tca cct gaa aca gtt gac agt gtg att atg ggc aat gtc ctg 258
Lys Val Ser Pro Glu Thr Val Asp Ser Val Ile Met Gly Asn Val Leu
45 50 55
cag agt tct tca gat gct ata tat ttg gca agg cat gtt ggt ttg cgt 306

Gln	Ser	Ser	Ser	Asp	Ala	Ile	Tyr	Leu	Ala	Arg	His	Val	Gly	Leu	Arg	
	60						65					70				
gtg	gga	atc	cca	aag	gag	acc	cca	gct	ctc	acg	att	aat	agg	ctc	tgt	354
Val	Gly	Ile	Pro	Lys	Glu	Thr	Pro	Ala	Leu	Thr	Ile	Asn	Arg	Leu	Cys	
	75						80					85				
ggg	tct	ggg	ttt	cag	tcc	att	gtg	aat	gga	tgt	cag	gaa	att	tgt	gtt	402
Gly	Ser	Gly	Phe	Gln	Ser	Ile	Val	Asn	Gly	Cys	Gln	Glu	Ile	Cys	Val	
	90					95					100				105	
aaa	gaa	gct	gaa	gtt	gtt	tta	tgt	gga	gga	acc	gaa	agc	atg	agc	caa	450
Lys	Glu	Ala	Glu	Val	Val	Leu	Cys	Gly	Gly	Thr	Glu	Ser	Met	Ser	Gln	
				110						115					120	
gct	ccc	tac	tgt	gtc	aga	aat	gtg	cgt	ttt	gga	acc	aag	ctt	gga	tca	498
Ala	Pro	Tyr	Cys	Val	Arg	Asn	Val	Arg	Phe	Gly	Thr	Lys	Leu	Gly	Ser	
			125					130					135			
gat	atc	aag	ctg	gaa	gat	tct	tta	tgg	gta	tca	tta	aca	gat	cag	cat	546
Asp	Ile	Lys	Leu	Glu	Asp	Ser	Leu	Trp	Val	Ser	Leu	Thr	Asp	Gln	His	
		140					145					150				
gtc	cag	ctc	ccc	atg	gca	atg	act	gca	gag	aat	ctt	gct	gta	aaa	cac	594
Val	Gln	Leu	Pro	Met	Ala	Met	Thr	Ala	Glu	Asn	Leu	Ala	Val	Lys	His	
	155					160					165					
aaa	ata	agc	aga	gaa	gaa	tgt	gac	aaa	tat	gcc	ctg	cag	tca	cag	cag	642
Lys	Ile	Ser	Arg	Glu	Glu	Cys	Asp	Lys	Tyr	Ala	Leu	Gln	Ser	Gln	Gln	
	170				175				180					185		
aga	tgg	aaa	gct	gct	aat	gat	gct	ggc	tac	ttt	aat	gat	gaa	atg	gca	690
Arg	Trp	Lys	Ala	Ala	Asn	Asp	Ala	Gly	Tyr	Phe	Asn	Asp	Glu	Met	Ala	
			190					195						200		
cca	att	gaa	gtg	aag	aca	aag	aaa	gga	aaa	cag	aca	atg	cag	gta	gac	738
Pro	Ile	Glu	Val	Lys	Thr	Lys	Lys	Gly	Lys	Gln	Thr	Met	Gln	Val	Asp	
		205						210					215			
gag	cat	gct	cgg	ccc	caa	acc	acc	ctg	gaa	cag	tta	cag	aaa	ctt	cct	786
Glu	His	Ala	Arg	Pro	Gln	Thr	Thr	Leu	Glu	Gln	Leu	Gln	Lys	Leu	Pro	
		220					225					230				
cca	gta	ttc	aag	aaa	gat	gga	act	gtt	act	gca	ggg	aat	gca	tcg	ggg	834
Pro	Val	Phe	Lys	Lys	Asp	Gly	Thr	Val	Thr	Ala	Gly	Asn	Ala	Ser	Gly	
	235					240					245					
gta	gct	gat	ggg	gct	gga	gct	gtt	atc	ata	gct	agt	gaa	gat	gct	gtt	882
Val	Ala	Asp	Gly	Ala	Gly	Ala	Val	Ile	Ile	Ala	Ser	Glu	Asp	Ala	Val	
	250				255					260				265		
aag	aaa	cat	aac	ttc	aca	cca	ctg	gca	aga	att	gtg	ggc	tac	ttt	gta	930
Lys	Lys	His	Asn	Phe	Thr	Pro	Leu	Ala	Arg	Ile	Val	Gly	Tyr	Phe	Val	
			270						275					280		
tct	gga	tgt	gat	ccc	tct	atc	atg	ggg	att	ggg	cct	gtc	cct	gct	atc	978
Ser	Gly	Cys	Asp	Pro	Ser	Ile	Met	Gly	Ile	Gly	Pro	Val	Pro	Ala	Ile	
		285						290					295			
agt	ggg	gca	ctg	aag	aaa	gca	gga	ctg	agt	ctt	aag	gac	atg	gat	ttg	1026
Ser	Gly	Ala	Leu	Lys	Lys	Ala	Gly	Leu	Ser	Leu	Lys	Asp	Met	Asp	Leu	
	300					305						310				
gta	gag	gtg	aat	gaa	gct	ttt	gct	ccc	cag	tac	ttg	gct	gtt	gag	agg	1074
Val	Glu	Val	Asn	Glu	Ala	Phe	Ala	Pro	Gln	Tyr	Leu	Ala	Val	Glu	Arg	
	315					320					325					
agt	ttg	gat	ctt	gac	ata	agt	aaa	acc	aat	gtg	aat	gga	gga	gcc	att	1122
Ser	Leu	Asp	Leu	Asp	Ile	Ser	Lys	Thr	Asn	Val	Asn	Gly	Gly	Ala	Ile	
	330				335					340				345		
gct	ttg	ggg	cac	cca	ctg	gga	gga	tct	gga	tca	aga	att	act	gca	cac	1170
Ala	Leu	Gly	His	Pro	Leu	Gly	Gly	Ser	Gly	Ser	Arg	Ile	Thr	Ala	His	
			350					355					360			
ctg	gtt	cac	gaa	tta	agg	cgt	cga	ggg	gga	aaa	tat	gcc	gtt	gga	tca	1218
Leu	Val	His	Glu	Leu	Arg	Arg	Arg	Gly	Gly	Lys	Tyr	Ala	Val	Gly	Ser	
		365					370					375				
gct	tgc	att	gga	ggg	ggc	caa	ggg	att	gct	gtc	atc	att	cag	agc	aca	1266

Ala Cys Ile Gly Gly Gly Gln Gly Ile Ala Val Ile Ile Gln Ser Thr
 380 385 390
 gcc tgaagagacc agtgagctca ctgtgaccca tccttactct acttggccag 1319
 Ala
 gccacagtaa aacaagtgac cttcagagca gctgccacaa ctggccatgc cctgccattg 1379
 aaacagtgat taagtttgat caagccatgg tgacacaaaa atgcattgat catgaatagg 1439
 agcccatgct agaagtacat tctctcagat ttgaaccagt gaaatatgat gtattttctga 1499
 gctaaaaactc aactatagaa gacattaaaa gaaatcgtat tcttgccaag taaccaccac 1559
 ttctgcctta gataatatga ttataaggaa atcaaataaa tgttgccotta acttcaaaca 1619
 aaaaaaaaaa aaaaaa 1634

<210> 76
 <211> 394
 <212> PRT
 <213> Homo sapiens

<400> 76
 Met Met Gly Val Phe Val Val Ala Ala Lys Arg Thr Pro Phe Gly Ala
 1 5 10 15
 Tyr Gly Gly Leu Leu Lys Asp Phe Thr Ala Thr Asp Leu Ser Glu Phe
 20 25 30
 Ala Ala Lys Ala Ala Leu Ser Ala Gly Lys Val Ser Pro Glu Thr Val
 35 40 45
 Asp Ser Val Ile Met Gly Asn Val Leu Gln Ser Ser Ser Asp Ala Ile
 50 55 60
 Tyr Leu Ala Arg His Val Gly Leu Arg Val Gly Ile Pro Lys Glu Thr
 65 70 75 80
 Pro Ala Leu Thr Ile Asn Arg Leu Cys Gly Ser Gly Phe Gln Ser Ile
 85 90 95
 Val Asn Gly Cys Gln Glu Ile Cys Val Lys Glu Ala Glu Val Val Leu
 100 105 110
 Cys Gly Gly Thr Glu Ser Met Ser Gln Ala Pro Tyr Cys Val Arg Asn
 115 120 125
 Val Arg Phe Gly Thr Lys Leu Gly Ser Asp Ile Lys Leu Glu Asp Ser
 130 135 140
 Leu Trp Val Ser Leu Thr Asp Gln His Val Gln Leu Pro Met Ala Met
 145 150 155 160
 Thr Ala Glu Asn Leu Ala Val Lys His Lys Ile Ser Arg Glu Glu Cys
 165 170 175
 Asp Lys Tyr Ala Leu Gln Ser Gln Gln Arg Trp Lys Ala Ala Asn Asp
 180 185 190
 Ala Gly Tyr Phe Asn Asp Glu Met Ala Pro Ile Glu Val Lys Thr Lys
 195 200 205
 Lys Gly Lys Gln Thr Met Gln Val Asp Glu His Ala Arg Pro Gln Thr
 210 215 220
 Thr Leu Glu Gln Leu Gln Lys Leu Pro Pro Val Phe Lys Lys Asp Gly
 225 230 235 240
 Thr Val Thr Ala Gly Asn Ala Ser Gly Val Ala Asp Gly Ala Gly Ala
 245 250 255
 Val Ile Ile Ala Ser Glu Asp Ala Val Lys Lys His Asn Phe Thr Pro
 260 265 270
 Leu Ala Arg Ile Val Gly Tyr Phe Val Ser Gly Cys Asp Pro Ser Ile
 275 280 285
 Met Gly Ile Gly Pro Val Pro Ala Ile Ser Gly Ala Leu Lys Lys Ala
 290 295 300
 Gly Leu Ser Leu Lys Asp Met Asp Leu Val Glu Val Asn Glu Ala Phe
 305 310 315 320
 Ala Pro Gln Tyr Leu Ala Val Glu Arg Ser Leu Asp Leu Asp Ile Ser
 325 330 335
 Lys Thr Asn Val Asn Gly Gly Ala Ile Ala Leu Gly His Pro Leu Gly

340 345 350
 Gly Ser Gly Ser Arg Ile Thr Ala His Leu Val His Glu Leu Arg Arg
 355 360 365
 Arg Gly Gly Lys Tyr Ala Val Gly Ser Ala Cys Ile Gly Gly Gly Gln
 370 375 380
 Gly Ile Ala Val Ile Ile Gln Ser Thr Ala
 385 390

<210> 77
 <211> 1642
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..68

<220>
 <221> CDS
 <222> 69..875

<220>
 <221> 3'UTR
 <222> 876..1642

<220>
 <221> polyA_signal
 <222> 1599..1604

<220>
 <221> polyA_site
 <222> 1627..1642

<400> 77
 attttatagc ggccgcgggc ggccgcggca gcggttgag gttgtaggac cggcgaggaa 60
 taggaatc atg gcg gct gcg ctg ttc gtg ctg ctg gga ttc gcg ctg ctg 110
 Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu
 -20 -15 -10
 ggc acc cac gga gcc tcc ggg gct gcc ggc aca gtc ttc act acc gta 158
 Gly Thr His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val
 -5 1 5 10
 gaa gac ctt ggc tcc aag ata ctc ctc acc tgc tcc ttg aat gac agc 206
 Glu Asp Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser
 15 20 25
 gcc aca gag gtc aca ggg cac cgc tgg ctg aag ggg ggc gtg gtg ctg 254
 Ala Thr Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu
 30 35 40
 aag gag gac gcg ctg ccc ggc cag aaa acg gag ttc aag gtg gac tcc 302
 Lys Glu Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser
 45 50 55
 gac gac cag tgg gga gag tac tcc tgc gtc ttc ctc ccc gag ccc atg 350
 Asp Asp Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met
 60 65 70
 ggc acg gcc aac atc cag ctc cac ggg cct ccc aga gtg aag gcc gtg 398
 Gly Thr Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val
 75 80 85 90
 aag tcg tca gaa cac atc aac gag ggg gag acg gcc atg ctg gtc tgc 446
 Lys Ser Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys
 95 100 105
 aag tca gag tcc gtg cca cct gtc act gac tgg gcc tgg tac aag atc 494

Lys Ser Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile
 110 115 120
 act gac tct gag gac aag gcc ctc atg aac ggc tcc gag agc agg ttc 542
 Thr Asp Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe
 125 130 135
 ttc gtg agt tcc tcg cag ggc ctg tca gag cta cac att gag aac ctg 590
 Phe Val Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu
 140 145 150
 aac atg gag gcc gac ccc ggc cag tac cgg tgc aac ggc acc agc tcc 638
 Asn Met Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser
 155 160 165 170
 aag ggc tcc gac cag gcc atc atc acg ctc cgc gtg cgc agc cac ctg 686
 Lys Gly Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu
 175 180 185
 gcc gcc ctc tgg ccc ttc ctg ggc atc gtg gct gag gtg ctg gtg ctg 734
 Ala Ala Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu
 190 195 200
 gtc acc atc atc ttc atc tac gag aag cgc cgg aag ccc gag gac gtc 782
 Val Thr Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val
 205 210 215
 ctg gat gat gac gac gcc ggc tct gca ccc ctg aag agc agc ggg cag 830
 Leu Asp Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln
 220 225 230
 cac cag aat gac aaa ggc aag aac gtc cgc cag agg aac tct tcc 875
 His Gln Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
 235 240 245
 tgaggcaggt ggcccgagga cgctccctgc tccgcgtctg cgccgcccgc ggagtccact 935
 cccagtgcctt gcaagattcc aagttctcac ctcttaaaga aaaccacccc cgtagattcc 995
 catcatcac ttccttcttt tttaaaaaag ttgggttttc tccattcagg attctgttcc 1055
 ttaggatttt ttccttctga agtggtttcac gagagcccgg gagctgctgc cctgcggccc 1115
 cgtctgtggc tttcagcctc tgggtctgag tcatggccgg gtgggcggca cagccttctc 1175
 cactggccgg agtcagtgcc aggtccttgc cctttgtgga aagtcacagg tcacacgagg 1235
 ggccccgtgt cctgcctgtc tgaagccaat gctgtctggt tgcgccattt ttgtgctttt 1295
 atgtttaatt ttatgagggc cacgggtctg tgttcgactc agcctcaggg acgactctga 1355
 cctcttgccc acagaggact cacttgccca caccgagggc gaccccgta cagcctcaag 1415
 tcaactccaa gcccctcct tgtctgtgca tccgggggca gctctggagg gggtttctg 1475
 gggaactggc gccatcgccg ggactccaga accgcagaag cctccccagc tcacccctgg 1535
 aggacggccg gctctctata gcaccagggc tcacgtggga acccccctcc caccacccgc 1595
 cacaataaag atcgccccca cctccaccct caaaaaaaaa aaaaaaa 1642

<210> 78
 <211> 269
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..21

<400> 78
 Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu Gly Thr
 -20 -15 -10
 His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
 -5 1 5 10
 Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr
 15 20 25
 Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu
 30 35 40
 Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp
 45 50 55

Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr
 60 65 70 75
 Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser
 80 85 90
 Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser
 95 100 105
 Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp
 110 115 120
 Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val
 125 130 135
 Ser Ser Ser Gln Gly Leu Ser Glu Leu His Ile Glu Asn Leu Asn Met
 140 145 150 155
 Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly
 160 165 170
 Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala
 175 180 185
 Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr
 190 195 200
 Ile Ile Phe Ile Tyr Glu Lys Arg Arg Lys Pro Glu Asp Val Leu Asp
 205 210 215
 Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln
 220 225 230 235
 Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
 240 245

<210> 79

<211> 1466

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

<222> 1..343

<220>

<221> CDS

<222> 344..1144

<220>

<221> 3'UTR

<222> 1145..1466

<400> 79
 attgtgactt tgggccaggc tgggggaaat gacccgggag ggtcccatgc ggctacataa 60
 aattggcagc cttagaacta gtgggaaggc ggggtgcgcga agtcgagggg cggagagagg 120
 gggccggagg agctgctttc tgaatccaag ttcgtgggct ctctcagaag tcctcaggac 180
 ggagcagagg tggccggcgg gcccggtga ctgcgcctyt gctttctttc cataaccttt 240
 tctttcggac tcgaatcacg gctgctgcga aggtctagt tccggacact agggtgcccg 300
 aacgcgctga tgccccgagt gctcgcaggc cttcccgtta acc atg ctg ccg ccg 355
 Met Leu Pro Pro
 ccg cgg ccc gca gct gcc ttg gcg ctg cct gtg ctc ctg cta ctg ctg 403
 Pro Arg Pro Ala Ala Leu Ala Leu Pro Val Leu Leu Leu Leu Leu
 -25 -20 -15 -10
 gtg gtg ctg acg ccg ccc ccg acc ggc gca agg cca tcc cca ggc cca 451
 Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro Ser Pro Gly Pro
 -5 1 5
 gat tac ctg cgg cgc gcc tgg atg cgg ctg cta gcg gag ggc gag gcc 499
 Asp Tyr Leu Arg Arg Gly Trp Met Arg Leu Leu Ala Glu Gly Glu Gly
 10 15 20
 tgc gct ccc tgc cgg cca gaa gag tgc gcc gcg ccg cgg ggc tgc ctg 547

Cys	Ala	Pro	Cys	Arg	Pro	Glu	Glu	Cys	Ala	Ala	Pro	Arg	Gly	Cys	Leu		
25						30					35						
gcg	ggc	agg	gtg	cgc	gac	gcg	tgc	ggc	tgc	tgc	tgg	gaa	tgc	gcc	aac	595	
Ala	Gly	Arg	Val	Arg	Asp	Ala	Cys	Gly	Cys	Cys	Trp	Glu	Cys	Ala	Asn		
40					45					50					55		
ctc	gag	ggc	cag	ctc	tgc	gac	ctg	gac	ccc	agt	gct	cac	ttc	tac	ggg	643	
Leu	Glu	Gly	Gln	Leu	Cys	Asp	Leu	Asp	Pro	Ser	Ala	His	Phe	Tyr	Gly		
				60					65						70		
cac	tgc	ggc	gag	cag	ctt	gag	tgc	cgg	ctg	gac	aca	ggc	ggc	gac	ctg	691	
His	Cys	Gly	Glu	Gln	Leu	Glu	Cys	Arg	Leu	Asp	Thr	Gly	Gly	Asp	Leu		
			75					80									
agc	cgc	gga	gag	gtg	ccg	gaa	cct	ctg	tgt	gcc	tgt	cgt	tcg	cag	agt	739	
Ser	Arg	Gly	Glu	Val	Pro	Glu	Pro	Leu	Cys	Ala	Cys	Arg	Ser	Gln	Ser		
		90					95					100					
ccg	ctc	tgc	ggg	tcc	gac	ggt	cac	acc	tac	tcc	cag	atc	tgc	cgc	ctg	787	
Pro	Leu	Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Gln	Ile	Cys	Arg	Leu		
	105					110					115						
cag	gag	gcg	gcc	cgc	gct	cgg	ccc	gat	gcc	aac	ctc	act	gtg	gca	cac	835	
Gln	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Asp	Ala	Asn	Leu	Thr	Val	Ala	His		
120					125					130					135		
ccg	ggg	ccc	tgc	gaa	tcg	ggg	ccc	cag	atc	gtg	tca	cat	cca	tat	gac	883	
Pro	Gly	Pro	Cys	Glu	Ser	Gly	Pro	Gln	Ile	Val	Ser	His	Pro	Tyr	Asp		
				140				145						150			
act	tgg	aat	gtg	aca	ggg	cag	gat	gtg	atc	ttt	ggc	tgt	gaa	gtg	ttt	931	
Thr	Trp	Asn	Val	Thr	Gly	Gln	Asp	Val	Ile	Phe	Gly	Cys	Glu	Val	Phe		
			155					160					165				
gcc	tac	ccc	atg	gcc	tcc	atc	gag	tgg	agg	aag	gat	ggc	ttg	gac	atc	979	
Ala	Tyr	Pro	Met	Ala	Ser	Ile	Glu	Trp	Arg	Lys	Asp	Gly	Leu	Asp	Ile		
		170				175					180						
cag	ctg	cca	ggg	gat	gac	ccc	cac	atc	tct	gtg	cag	ttt	agg	ggt	gga	1027	
Gln	Leu	Pro	Gly	Asp	Asp	Pro	His	Ile	Ser	Val	Gln	Phe	Arg	Gly	Gly		
		185				190					195						
ccc	cag	agg	ttt	gag	gtg	act	ggc	tgg	ctg	cag	atc	cag	gct	gtg	cgt	1075	
Pro	Gln	Arg	Phe	Glu	Val	Thr	Gly	Trp	Leu	Gln	Ile	Gln	Ala	Val	Arg		
					205				210					215			
ccc	agt	gat	gag	ggc	act	tac	cgc	tgc	ctt	ggc	cca	atg	ccc	tgg	gtc	1123	
Pro	Ser	Asp	Glu	Gly	Thr	Tyr	Arg	Cys	Leu	Gly	Pro	Met	Pro	Trp	Val		
				220				225					230				
aag	tgg	agg	ccc	ctg	cta	gct	tgacagt	gct	cacacctgac	cagctgaact						1174	
Lys	Trp	Arg	Pro	Leu	Leu	Ala											
			235														
ctacaggcat	ccccagctg	cgatcactaa	acctggttcc	tgaggaggag	gctgagagtg	1234											
aagagaatga	cgattactac	taggtccaga	gctctggccc	atgggggtgg	gtgagcggct	1294											
atagtgttca	tccctgctct	tgaaaagacc	tggaaagggg	agcagggtcc	cttcacgac	1354											
tgctttcatg	ctgtcagtag	ggatgatcat	gggaggccta	tttgactcca	aggtagcagt	1414											
gtggtaggat	agagacaaaa	gctggaggag	ggtagggaga	gaagctgaga	cc	1466											

<210> 80
 <211> 267
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> SIGNAL
 <222> 1..30

 <400> 80
 Met Leu Pro Pro Pro Arg Pro Ala Ala Ala Leu Ala Leu Pro Val Leu
 -30 -25 -20 -15
 Leu Leu Leu Leu Val Val Leu Thr Pro Pro Pro Thr Gly Ala Arg Pro

				-10					-5					1			
Ser	Pro	Gly	Pro	Asp	Tyr	Leu	Arg	Arg	Gly	Trp	Met	Arg	Leu	Leu	Ala		
		5					10					15					
Glu	Gly	Glu	Gly	Cys	Ala	Pro	Cys	Arg	Pro	Glu	Glu	Cys	Ala	Ala	Pro		
	20					25					30						
Arg	Gly	Cys	Leu	Ala	Gly	Arg	Val	Arg	Asp	Ala	Cys	Gly	Cys	Cys	Trp		
35				40					45						50		
Glu	Cys	Ala	Asn	Leu	Glu	Gly	Gln	Leu	Cys	Asp	Leu	Asp	Pro	Ser	Ala		
			55					60						65			
His	Phe	Tyr	Gly	His	Cys	Gly	Glu	Gln	Leu	Glu	Cys	Arg	Leu	Asp	Thr		
		70					75						80				
Gly	Gly	Asp	Leu	Ser	Arg	Gly	Glu	Val	Pro	Glu	Pro	Leu	Cys	Ala	Cys		
	85					90					95						
Arg	Ser	Gln	Ser	Pro	Leu	Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Gln		
	100				105					110							
Ile	Cys	Arg	Leu	Gln	Glu	Ala	Ala	Arg	Ala	Arg	Pro	Asp	Ala	Asn	Leu		
115				120					125					130			
Thr	Val	Ala	His	Pro	Gly	Pro	Cys	Glu	Ser	Gly	Pro	Gln	Ile	Val	Ser		
			135					140					145				
His	Pro	Tyr	Asp	Thr	Trp	Asn	Val	Thr	Gly	Gln	Asp	Val	Ile	Phe	Gly		
		150				155						160					
Cys	Glu	Val	Phe	Ala	Tyr	Pro	Met	Ala	Ser	Ile	Glu	Trp	Arg	Lys	Asp		
	165					170				175							
Gly	Leu	Asp	Ile	Gln	Leu	Pro	Gly	Asp	Asp	Pro	His	Ile	Ser	Val	Gln		
	180				185					190							
Phe	Arg	Gly	Gly	Pro	Gln	Arg	Phe	Glu	Val	Thr	Gly	Trp	Leu	Gln	Ile		
195				200					205					210			
Gln	Ala	Val	Arg	Pro	Ser	Asp	Glu	Gly	Thr	Tyr	Arg	Cys	Leu	Gly	Pro		
			215				220						225				
Met	Pro	Trp	Val	Lys	Trp	Arg	Pro	Leu	Leu	Ala							
		230					235										

<210> 81
 <211> 1406
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..26

 <220>
 <221> CDS
 <222> 27..689

<220>
 <221> 3'UTR
 <222> 690..1406

<220>
 <221> polyA_signal
 <222> 1302..1307

<220>
 <221> polyA_site
 <222> 1325..1406

<400> 81
 cccggaagtgcgcaggcgctggcaagatggcgggagggtgcgc ccgctgcgg 53
 MetAlaGlyGlyValArgProLeuArg

<220>
 <221> SIGNAL
 <222> 1..32

<400> 82
 Met Ala Gly Gly Val Arg Pro Leu Arg Gly Leu Arg Ala Leu Cys Arg
 -30 -25 -20
 Val Leu Leu Phe Leu Ser Gln Phe Cys Ile Leu Ser Gly Gly Glu Ser
 -15 -10 -5
 Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys
 1 5 10 15
 Ser Arg Leu Pro Ala Asp Cys Ile Asp Cys Thr Thr Asn Phe Ser Cys
 20 25 30
 Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Ala Val Lys Pro Ser Val
 35 40 45
 Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Asn Phe Ile Ile Asn
 50 55 60
 Met Thr Cys Arg Phe Cys Trp Gln Leu Pro Glu Thr Asp Tyr Glu Cys
 65 70 75 80
 Thr Asn Ser Thr Ser Cys Met Thr Val Ser Cys Pro Arg Gln Arg Tyr
 85 90 95
 Pro Ala Asn Cys Thr Val Arg Asp His Val His Cys Leu Gly Asn Arg
 100 105 110
 Thr Phe Pro Lys Met Leu Tyr Cys Asn Trp Thr Gly Gly Tyr Lys Trp
 115 120 125
 Ser Thr Ala Leu Ala Leu Ser Ile Thr Leu Gly Gly Phe Gly Ala Asp
 130 135 140
 Arg Phe Tyr Leu Gly Gln Trp Arg Glu Gly Leu Gly Lys Leu Phe Ser
 145 150 155 160
 Phe Gly Gly Leu Gly Ile Trp Thr Leu Ile Asp Val Leu Leu Ile Gly
 165 170 175
 Val Gly Tyr Val Gly Pro Ala Asp Gly Ser Leu Tyr Ile
 180 185

<210> 83
 <211> 1754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..117

<220>
 <221> CDS
 <222> 118..510

<220>
 <221> 3'UTR
 <222> 511..1754

<220>
 <221> polyA_signal
 <222> 1718..1723

<220>
 <221> polyA_site
 <222> 1739..1754

<400> 83

tccccggccg	ccgccgttgc	gctcgccgcg	ctcgactga	agccccggcc	ctcgcgccg	60
gcggttcgcc	ccgcagcctc	gccccctgcc	caccggggcg	gccgtagggc	ggtcacg	117
atg ctg ccg	ccc tta ccc	tcc cgc ctc	ggg ctg ctg	ctg ctg ctg	ctc	165
Met Leu Pro	Pro Leu Pro	Ser Arg	Leu Gly Leu	Leu Leu Leu	Leu Leu	
	-20		-15		-10	
ctg tgc ccg	gcg cac gtc	ggc gga ctg	tgg tgg gct	gtg ggc agc	ccc	213
Leu Cys Pro	Ala His Val	Gly Leu Trp	Trp Ala Val	Gly Ser Pro		
	-5	1	5			
ttg gtt atg	gac cct acc	agc atc tgc	agg aag gca	cgg cgg ctg	gcc	261
Leu Val Met	Asp Pro Thr	Ser Ile Cys	Arg Lys Ala	Arg Arg Leu	Ala	
10	15	20	25			
ggg cgg cag	gcc gag ttg	tgc cag gct	gag ccg gaa	gtg gtg gca	gag	309
Gly Arg Gln	Ala Glu Leu	Cys Gln Ala	Glu Pro Glu	Val Val Ala	Glu	
	30	35	40			
ctg gct ccg	ggc gcc cgg	ctc ggg gtg	cga gag tgc	cag ttc cag	ttc	357
Leu Ala Arg	Gly Ala Arg	Leu Gly Val	Arg Glu Cys	Gln Phe Gln	Phe	
	45	50	55			
cgc ttc cgc	cgc tgg aat	tgc tcc agc	cac agc aag	gcc ttt gga	cgc	405
Arg Phe Arg	Arg Trp Asn	Cys Ser Ser	His Ser Lys	Ala Phe Gly	Arg	
	60	65	70			
atc ctg caa	cag ggt cag	tgt ggg gag	ggg cac cct	gca agg acc	ctg	453
Ile Leu Gln	Gln Gly Gln	Cys Gly Glu	Gly His Pro	Ala Arg Thr	Leu	
	75	80	85			
cct ccc agg	ccc ctg ggg	cag ccc tcc	cgc cgc agg	ttt cag gtc	cca	501
Pro Pro Arg	Pro Leu Gln	Pro Ser Arg	Arg Arg Phe	Gln Val Pro		
90	95	100	105			
ggc ccc agc	tgaccgcccc	agccccgcgt	gattgcacct	gtctgcattc		550
Gly Pro Ser						
acagacattc	gggagacggc	cttcgtgttc	gccatcactg	cggccggcgc	cagccacgcc	610
gtcacgcagg	cctgttctat	gggcagactg	ctgcagtgcg	gctgccaggc	gccccgcggg	670
cgggccccctc	cccggccctc	cggcctgccc	ggcaccctcg	gaccccttg	ccccgcgggc	730
tccccggaag	gcagcgccgc	ctgggagtgg	ggaggctgcg	gcgacgacgt	ggacttcggg	790
gacgagaagt	cgaggctctt	tatgsacgcg	cggcacaagc	ggggacgcgg	agacatccgc	850
gcgttggtgc	aactgcacaa	caacgaggcg	ggcaggctgg	ccgtgcggag	ccacacgcgc	910
accgagtgc	aatgccacgg	gctgtcggga	tcatgcgcgc	tgcgcacctg	ctggcagaag	970
ctgcctccat	ttcgcgaggt	gggcgcgcgg	ctgctggagc	gcttcacagg	cgcctcacgc	1030
gtcatgggca	ccaacgacgg	caaggccctg	ctgcccgcgg	tccgcacgct	caagccgccc	1090
ggccgagcgg	acctcctcta	cgccgccgat	tcgcccgaact	tctgcgcccc	caaccgacgc	1150
accggctccc	ccggcacgcg	cggtcgcgcc	tgcaatagca	gcgccccgga	cctcagcggc	1210
tgcgacctgc	tgtgctgcgg	ccgcgggcac	cgccaggaga	gcgtgcagct	cgaagagaac	1270
tgccctgtgcc	gcttcactg	gtgctgcgta	gtacagtgcc	accgctgccg	tgtgcgcaag	1330
gagctcagcc	tctgctgtg	acccgccgcc	cggccgctag	actgacttcg	cgcagcgggtg	1390
gctcgcaact	gtgggacctc	agggcacccg	caccgggcgc	ctctcgccgc	tcgagcccag	1450
cctctccctg	ccaaagccca	actcccagg	ctctggaaat	ggtgaggcga	ggggcttgag	1510
aggaacgccc	accacgaag	gcccagggcg	ccagacggcc	ccgaaaaggc	gctcggggag	1570
cgtttaaagg	acactgtaca	ggccctccct	ccccttggcc	tctaggagga	aacagttttt	1630
tagactggaa	aaaagccagt	ctaaaggcct	ctggatactg	ggctccccag	aactgctggc	1690
cacaggatgg	tgggtgaggt	tagtatcaat	aaagatattt	aaaccaccaa	aaaaaaaaaa	1750
aaaa						1754

<210> 84

<211> 131

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..24

<400> 84
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
-20 -15 -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
25 30 35 40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
45 50 55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
60 65 70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
75 80 85
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
90 95 100
Gly Pro Ser
105

<210> 85
<211> 1754
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..117

<220>
<221> CDS
<222> 118..510

<220>
<221> 3'UTR
<222> 511..1754

<220>
<221> polyA_signal
<222> 1718..1723

<220>
<221> polyA_site
<222> 1739..1754

<400> 85
tccccggccg ccgcccgttgc gctcgccgcg ctcgcactga agcccggggcc ctgcgcgcgc 60
gcgggttcgcc ccgcagcctc gcccctgcc caccgggcg gccgtagggc ggtaacg 117
atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
-20 -15 -10
ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
-5 1 5
ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
10 15 20 25
ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
30 35 40

```

ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
      45                      50                      55
cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60                      65                      70
atc ctg caa cag ggt cag tgt ggg gag ggg cac cct gca agg acc ctg 453
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
      75                      80                      85
cct ccc agg ccc ctg ggg cag ccc tcc cgc cgc agg ttt cag gtc cca 501
Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
      90                      95                      100                      105
ggc ccc agc tgaccgcccc agcccgcgct gattgcacct gtctgcattc 550
Gly Pro Ser
acagacattc gggagacggc cttcgtgttc gccatcactg cggccggcgc cagccacgcc 610
gtcacgcagg cctgttctat gggcgagctg ctgcagtgcg gctgccaggc gccccgcggg 670
cgggccccctc cccggccctc cggcctgccc ggcacccccg gacccccctgg ccccgcgggc 730
tccccggaag gcagcgccgc ctgggagtgg ggaggctgcg gcgacgacgt ggacttcggg 790
gacgagaagt cgaggctctt tatggacgcg cggcacaagc ggggacgcgg agacatccgc 850
gcgttggtgc aactgcacaa caacgaggcg ggcaggctgg ccgtgcggag ccacacgcgc 910
accgagtga aatgccacgg gctgtcggga tcatgcgcgc tgcgcacctg ctggcagaag 970
ctgcctccat ttcgcgaggt gggcgcgcg ctgctggagc gcttycacgg cgcctcacgc 1030
gtcatgggca ccaacgacgg caaggccctg ctgcccgccg tccgcacgct caagccgccg 1090
ggccgagcgg acctcctcta cgcccgccat tgcgccgact tctgcgcccc caaccgacgc 1150
accggtccc cgggcacgcg cggtcgcgcc tgcaatagca gcgccccgga cctcagcggc 1210
tgcgacctgc tgtgtgcgg ccgcgggcac cgccaggaga gcgtgcagct cgaagagaac 1270
tgccgtgtgc gcttccactg gtgctgcgta gtacagtgcc accgctgccg tgtgcgcaag 1330
gagctcagcc tctgcctgtg acccgccgcc cggccgctag actgacttcg cgcagcgggtg 1390
gctcgcacct gtgggacctc agggcaccgg caccggggcg ctctcgccgc tcgagcccag 1450
cctctccctg ccaaagccca actcccaggg ctctggaaat ggtgaggcga ggggcttag 1510
aggaacgccc acccaggaag gccagggcg ccagacggcc ccgaaaaggc gtcggggag 1570
cgtttaaagg aactgtaca ggccctccct ccccttgcc tctaggagga aacagttttt 1630
tagactggaa aaaagccagt ctaaaggcct ctggatactg ggctccccag aactgctggc 1690
cacaggatgg tgggtgaggt tagtatcaat aaagatatatt aaaccaccaa aaaaaaaaaa 1750
aaaa
1754

```

<210> 86
<211> 131
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..24

```

<400> 86
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
      -20                      -15                      -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
      -5                      1                      5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
      10                      15                      20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
      25                      30                      35                      40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
      45                      50                      55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60                      65                      70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly His Pro Ala Arg Thr Leu
      75                      80                      85

```

```

Pro Pro Arg Pro Leu Gly Gln Pro Ser Arg Arg Arg Phe Gln Val Pro
  90                      95                      100
Gly Pro Ser
105

<210> 87
<211> 1431
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..151

<220>
<221> CDS
<222> 152..655

<220>
<221> 3'UTR
<222> 656..1431

<220>
<221> polyA_signal
<222> 1399..1404

<220>
<221> polyA_site
<222> 1416..1431

<400> 87
aatttttttct cacaaggact ggggtgaagag ttctgcagcc ttacagagac tggaaaagaa 60
gcccaaacca agggccccag agagggtcccc caggcccctt tgggtccctg agcctcagct 120
ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
                                Met Leu Phe Arg Leu Ser Glu
                                1 5
cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
10 15 20
gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
25 30 35
cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
40 45 50 55
tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
60 65 70
ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
75 80 85
gaa gag gag gat gat gaa gaa gag gaa gaa gag gac agc cag gct 460
Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
90 95 100
gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
105 110 115
ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
120 125 130 135

```

tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
 Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
 140 145 150
 agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
 Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
 155 160 165
 aca taggcaccca gcctgcatct cccaggagga agtggagggg acatcgctgt 705
 Thr
 tccccagaaa cccactctat cctcaccctg ttttgtgctc ttccctcgc ctgctagggc 765
 tgcggcttct gacttctaga agactaaggc tggctctgtgt ttgcttggtt gccacacctt 825
 ggctgatacc cagagaacct gggcacttgc tgcctgatgc ccaccctgc cagtcattcc 885
 tccattcacc cagcgggagg tgggatgtga gacagcccac attggaaaat ccagaaaacc 945
 gggaacaggg atttgccctt cacaattcta ctcccagat cctctccctt ggacacagga 1005
 gacccacagg gcaggaccct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065
 cttagatcct tttctacca ctttctatg gaggattcca agtcaccact tctctaccg 1125
 gcttctacca ggggtccagga ctaaggcgtt tttctccata gcctcaacat tttgggaatc 1185
 ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245
 tgttgctgtt tgtgcttga tggcaggaat gccgcctagt ttatgtcccc ggtggggcac 1305
 acagcggggg gcgccagggt ttccttgtcc cccagctgct ctgccccctt ccccttcttc 1365
 cctgactcca ggcctgaacc cctccctgct tgtaataaat ctttgtaaag aaaaaaaaaa 1425
 aaaaaa 1431

<210> 88
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 88
 Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser
 1 5 10 15
 Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
 20 25 30
 Pro Asn Pro Cys Ala Tyr Thr Pro Ser Leu Lys Ala Val Gln Arg
 35 40 45
 Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
 50 55 60
 Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
 65 70 75 80
 Pro Arg Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
 85 90 95
 Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
 100 105 110
 Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
 115 120 125
 Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
 130 135 140
 Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
 145 150 155 160
 Pro Ser Pro Ser Glu Pro Gly Thr
 165

<210> 89
 <211> 1431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..151

<220>
 <221> CDS
 <222> 152..655

<220>
 <221> 3'UTR
 <222> 656..1431

<220>
 <221> polyA_signal
 <222> 1399..1404

<220>
 <221> polyA_site
 <222> 1416..1431

<400> 89
 aatttttttct cacaaggact ggggtgaagag ttctgcagcc ttacagagac tggaaaagaa 60
 gcccaaacca agggccccag agaggtcccc caggcccctt tgggtccctg agcctcagct 120
 ggagatccgg cgcaggagac caacgcctgc c atg ctg ttc cgg ctc tca gag 172
 Met Leu Phe Arg Leu Ser Glu
 1 5
 cac tcc tca cca gag gag gaa gcc tcc ccc cac cag aga gcc tca gga 220
 His Ser Ser Pro Glu Glu Glu Ala Ser Pro His Gln Arg Ala Ser Gly
 10 15 20
 gag ggg cac cat ctc aag tcg aag aga ccc aac ccc tgt gcc tac aca 268
 Glu Gly His His Leu Lys Ser Lys Arg Pro Asn Pro Cys Ala Tyr Thr
 25 30 35
 cca cct tcg ctg aaa gct gtg cag cgc att gct gag tct cac ctg cag 316
 Pro Pro Ser Leu Lys Ala Val Gln Arg Ile Ala Glu Ser His Leu Gln
 40 45 50 55
 tct atc agc aat ttg aat gag aac cag gcc tca gag gag gag gat gag 364
 Ser Ile Ser Asn Leu Asn Glu Asn Gln Ala Ser Glu Glu Glu Asp Glu
 60 65 70
 ctg ggg gag ctt cgg gag ctg ggt tat cca aga gag gaa gat gag gag 412
 Leu Gly Glu Leu Arg Glu Leu Gly Tyr Pro Arg Glu Glu Asp Glu Glu
 75 80 85
 gaa gag gag gat gat gaa gaa gag gaa gaa gaa gag gac agc cag gct 460
 Glu Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu Glu Asp Ser Gln Ala
 90 95 100
 gaa gtc ctg aag gtc atc agg cag tct gct ggg caa aag aca acc tgt 508
 Glu Val Leu Lys Val Ile Arg Gln Ser Ala Gly Gln Lys Thr Thr Cys
 105 110 115
 ggc cag ggt ctg gaa ggg ccc tgg gag cgc cca ccc cct ctg gat gag 556
 Gly Gln Gly Leu Glu Gly Pro Trp Glu Arg Pro Pro Pro Leu Asp Glu
 120 125 130 135
 tcc gag aga gat gga ggc tct gag gac caa gtg gaa gac cca gca cta 604
 Ser Glu Arg Asp Gly Gly Ser Glu Asp Gln Val Glu Asp Pro Ala Leu
 140 145 150
 agt gag cct ggg gag gaa cct cag cgc cct tcc ccc tct gag cct ggc 652
 Ser Glu Pro Gly Glu Glu Pro Gln Arg Pro Ser Pro Ser Glu Pro Gly
 155 160 165
 aca taggcacca gcctgcatct cccaggagga agtggagggg acatcgctgt 705
 Thr
 tccccagaaa cccactctat cctcacccctg ttttgtgtctc ttcccctcgc ctgctagggc 765
 tgcggttct gacttctaga agactaaggc tgggtctgtgt ttgcttgttt gccacccctt 825
 ggctgatacc cagagaacct gggcacttgc tgcctgatgc ccaccctgc cagtcattcc 885
 tccattcacc cagcgggagg tgggatgtga gacagcccac attggaaaat ccagaaaacc 945
 gggaacaggg atttgccctt cacaattcta ctccccagat cctctcccct ggacacagga 1005
 gaccacagg gcaggaccct aagatctggg gaaaggaggt cctgagaacc ttgaggtacc 1065

```

cttagatcct tttctacca ctttcctatg gaggattcca agtcaccact tctctcaccg 1125
gcttctacca gggtcacagga ctaaggcggt tttctccata gcctcaacat tttgggaatc 1185
ttcccttaat cacccttgct cctcctgggt gcctggaaga tggactggca gagacctctt 1245
tggtgcggtt tgtgctttga tgccaggaat gccgcctagt ttatgtcccc ggtggggcac 1305
acagcggggg gcgccagggt ttccttgctc cccagctgct ctgccccttt ccccttcttc 1365
cctgactcca ggctgaacc cctcccgtgc tgtaataaat ctttgtaaag aaaaaaaaaa 1425
aaaaaa
1431

```

```

<210> 90
<211> 168
<212> PRT
<213> Homo sapiens

```

```

<400> 90
Met Leu Phe Arg Leu Ser Glu His Ser Ser Pro Glu Glu Glu Ala Ser
1      5      10      15
Pro His Gln Arg Ala Ser Gly Glu Gly His His Leu Lys Ser Lys Arg
20     25     30
Pro Asn Pro Cys Ala Tyr Thr Pro Pro Ser Leu Lys Ala Val Gln Arg
35     40     45
Ile Ala Glu Ser His Leu Gln Ser Ile Ser Asn Leu Asn Glu Asn Gln
50     55     60
Ala Ser Glu Glu Glu Asp Glu Leu Gly Glu Leu Arg Glu Leu Gly Tyr
65     70     75     80
Pro Arg Glu Glu Asp Glu Glu Glu Glu Asp Asp Glu Glu Glu Glu
85     90     95
Glu Glu Glu Asp Ser Gln Ala Glu Val Leu Lys Val Ile Arg Gln Ser
100    105    110
Ala Gly Gln Lys Thr Thr Cys Gly Gln Gly Leu Glu Gly Pro Trp Glu
115    120    125
Arg Pro Pro Pro Leu Asp Glu Ser Glu Arg Asp Gly Gly Ser Glu Asp
130    135    140
Gln Val Glu Asp Pro Ala Leu Ser Glu Pro Gly Glu Glu Pro Gln Arg
145    150    155    160
Pro Ser Pro Ser Glu Pro Gly Thr
165

```

```

<210> 91
<211> 1417
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..47

```

```

<220>
<221> CDS
<222> 48..1301

```

```

<220>
<221> 3'UTR
<222> 1302..1417

```

```

<220>
<221> polyA_signal
<222> 1360..1365

```

```

<220>
<221> polyA_site

```


<222> 1402..1417

<400> 91

```
ctcctcagct tcaggcacca ccactgacct gggacagtga atcgaca atg ccg tct      56
                                     Met Pro Ser
tct gtc tcg tgg ggc atc ctc ctg ctg gca ggc ctg tgc tgc ctg gtc      104
Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
-20          -15          -10          -5
cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc cag aag aca      152
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr
          1          5          10
gat aca tcc cac cat gat cag gat cac cca acc ttc aac aag atc acc      200
Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr
          15          20          25
ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag ctg gca cac      248
Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His
          30          35          40
cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc atc gct aca      296
Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr
          45          50          55          60
gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act cac gat gaa      344
Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu
          65          70          75
atc ctg gag agc ctg aat ttc aac ctc acg gag att ccg gag gct cag      392
Ile Leu Glu Ser Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala Gln
          80          85          90
atc cat gaa ggc ttc cag gaa ctc cgt acc ctc aac cag cca gac      440
Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp
          95          100          105
agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc agc gag ggc      488
Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly
          110          115          120
ctg aag cta gtg gat aag ttt ttg gag gat gtt aaa aag ttg tac cac      536
Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His
          125          130          135          140
tca gaa gcc ttc act gtc aac ttc ggg gac acc gaa gag gcc aag aaa      584
Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys
          145          150          155
cag atc aac gat tac gtg gag aag ggt act caa ggg aaa att gtg gat      632
Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp
          160          165          170
ttg gtc aag gag ctt gac aga gac aca gtt ttt gct ctg gtg aat tac      680
Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr
          175          180          185
atc ttc ttt aaa ggc aaa tgg gag aga ccc ttt gaa gtc aag gac acc      728
Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr
          190          195          200
gag gaa gag gac ttc cac gtg gac cag gcg acc acc gtg aag gtg cct      776
Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val Lys Val Pro
          205          210          215          220
atg atg aag cgt tta ggc atg ttt aac atc cag cac tgt aag aag ctg      824
Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu
          225          230          235
tcc agc tgg gtg ctg ctg atg aaa tac ctg ggc aat gcc acc gcc atc      872
Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile
          240          245          250
ttc ttc ctg cct gat gag ggg aaa cta cag cac ctg gaa aat gaa ctc      920
Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu
          255          260          265
acc cac gat atc atc acc aag ttc ctg gaa aat gaa gac aga agg tct      968
```

Thr	His	Asp	Ile	Ile	Thr	Lys	Phe	Leu	Glu	Asn	Glu	Asp	Arg	Arg	Ser		
270						275					280						
gcc	agc	tta	cat	tta	ccc	aaa	ctg	tcc	att	act	gga	acc	tat	gat	ctg	1016	
Ala	Ser	Leu	His	Leu	Pro	Lys	Leu	Ser	Ile	Thr	Gly	Thr	Tyr	Asp	Leu		
285					290					295					300		
aag	agc	gtc	ctg	ggg	caa	ctg	ggc	atc	act	aag	gtc	ttc	agc	aat	ggg	1064	
Lys	Ser	Val	Leu	Gly	Gln	Leu	Gly	Ile	Thr	Lys	Val	Phe	Ser	Asn	Gly		
				305					310					315			
gct	gac	ctc	tcc	ggg	gtc	aca	gag	gag	gca	ccc	ctg	aag	ctc	tcc	aag	1112	
Ala	Asp	Leu	Ser	Gly	Val	Thr	Glu	Glu	Ala	Pro	Leu	Lys	Leu	Ser	Lys		
			320				325						330				
gcc	gtg	cat	aag	gct	gtg	ctg	acc	atc	gac	gag	aaa	ggg	act	gaa	gct	1160	
Ala	Val	His	Lys	Ala	Val	Leu	Thr	Ile	Asp	Glu	Lys	Gly	Thr	Glu	Ala		
		335				340						345					
gct	ggg	gcc	atg	ttt	tta	gag	gcc	ata	ccc	atg	tct	atc	ccc	ccc	gag	1208	
Ala	Gly	Ala	Met	Phe	Leu	Glu	Ala	Ile	Pro	Met	Ser	Ile	Pro	Pro	Glu		
	350					355				360							
gtc	aag	ttc	aac	aaa	ccc	ttt	gtc	ttc	tta	atg	att	gaa	caa	aat	acc	1256	
Val	Lys	Phe	Asn	Lys	Pro	Phe	Val	Phe	Leu	Met	Ile	Glu	Gln	Asn	Thr		
365				370				375						380			
aag	tct	ccc	ctc	ttc	atg	gga	aaa	gtg	gtg	aat	ccc	acc	caa	aaa		1301	
Lys	Ser	Pro	Leu	Phe	Met	Gly	Lys	Val	Val	Asn	Pro	Thr	Gln	Lys			
			385					390					395				
taactgcctc	tcgctcctca	acccctcccc	tccatccctg	gccccctccc	tgatgacat	1361											
taaagaagg	gttgcctggt	ccctgcctgc	atgtgactgc	aaaaaaaaa	aaaaaa	1417											

<210> 92
 <211> 418
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..24

<400> 92

Met	Pro	Ser	Ser	Val	Ser	Trp	Gly	Ile	Leu	Leu	Leu	Ala	Gly	Leu	Cys		
				-20					-15						-10		
Cys	Leu	Val	Pro	Val	Ser	Leu	Ala	Glu	Asp	Pro	Gln	Gly	Asp	Ala	Ala		
			-5				1				5						
Gln	Lys	Thr	Asp	Thr	Ser	His	His	Asp	Gln	Asp	His	Pro	Thr	Phe	Asn		
	10				15					20							
Lys	Ile	Thr	Pro	Asn	Leu	Ala	Glu	Phe	Ala	Phe	Ser	Leu	Tyr	Arg	Gln		
	25			30				35						40			
Leu	Ala	His	Gln	Ser	Asn	Ser	Thr	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser		
			45					50						55			
Ile	Ala	Thr	Ala	Phe	Ala	Met	Leu	Ser	Leu	Gly	Thr	Lys	Ala	Asp	Thr		
		60					65					70					
His	Asp	Glu	Ile	Leu	Glu	Ser	Leu	Asn	Phe	Asn	Leu	Thr	Glu	Ile	Pro		
	75				80						85						
Glu	Ala	Gln	Ile	His	Glu	Gly	Phe	Gln	Glu	Leu	Leu	Arg	Thr	Leu	Asn		
	90			95						100							
Gln	Pro	Asp	Ser	Gln	Leu	Gln	Leu	Thr	Thr	Gly	Asn	Gly	Leu	Phe	Leu		
	105			110						115					120		
Ser	Glu	Gly	Leu	Lys	Leu	Val	Asp	Lys	Phe	Leu	Glu	Asp	Val	Lys	Lys		
			125					130						135			
Leu	Tyr	His	Ser	Glu	Ala	Phe	Thr	Val	Asn	Phe	Gly	Asp	Thr	Glu	Glu		
		140					145					150					
Ala	Lys	Lys	Gln	Ile	Asn	Asp	Tyr	Val	Glu	Lys	Gly	Thr	Gln	Gly	Lys		
	155					160						165					

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
 170 175 180
 Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
 185 190 195 200
 Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Ala Thr Thr Val
 205 210 215
 Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
 220 225 230
 Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
 235 240 245
 Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
 250 255 260
 Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 265 270 275 280
 Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 285 290 295
 Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 300 305 310
 Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 315 320 325
 Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 330 335 340
 Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 345 350 355 360
 Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 365 370 375
 Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 380 385 390
 Gln Lys

<210> 93
 <211> 1115
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..277

<220>
 <221> CDS
 <222> 278..733

<220>
 <221> 3'UTR
 <222> 734..1115

<220>
 <221> polyA_signal
 <222> 1072..1077

<220>
 <221> polyA_site
 <222> 1101..1115

<400> 93
 ctctttgctc taacagacag cagcgacttt aggctggata atagtcaa atcttacctcg 60
 ctctttcact gctagtaaga tcagattgcg tttctttcag ttactcttca atcgccagtt 120
 tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
 ggaaaaaaca aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240

gattttactt agatgattta cacaatgaag aaagtac atg cac ttt ggg ctt ctg 295
Met His Phe Gly Leu Leu
-15
tcc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat tct gag 343
Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu
-10 -5 1
gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca cca ctg 391
Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu
5 10 15 20
aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat agc cca tgt 439
Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Ser Pro Cys
25 30 35
aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga cag tgc 487
Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys
40 45 50
gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga ttt gaa 535
Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu
55 60 65
agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca aac agg 583
Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg
70 75 80
att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc ttt ttg 631
Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu
85 90 95 100
gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat ttt tat 679
Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr
105 110 115
aac aat cag aca aaa cat gtg aac gtt tca agt atg gtg gat gcc tgg 727
Asn Asn Gln Thr Lys His Val Asn Val Ser Ser Met Val Asp Ala Trp
120 125 130
gca ata tgaacaattt tgagacactg gaagaatgca agaacatttg tgaagatggt 783
Ala Ile
ccgaatggtt tccaggtgga taattatgga acccagctca atgctgtgaa taactccctg 843
actccgcaat caaccaaggt tcccagcctt tttgttacaa aagaaggaac aaatgatggt 903
tggaagaatg cggtcatat ttaccaagtc tttctgaacg ccttctgcat tcatgcatcc 963
atgttctttc taggattgga tagcatttca tgcctatggt aatattttgtg cttttggcat 1023
ttccttaata tttatatgta tacgtgatgc ctttgatagc atactgctaa taaagtttta 1083
atatttacat gcataggaaa aaaaaaaaaa aa 1115

<210> 94
<211> 152
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..19

<400> 94
Met His Phe Gly Leu Leu Ser Leu Leu Leu Asn Leu Ala Pro Ala Pro
-15 -10 -5
Leu Asn Ala Asp Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp
1 5 10
Thr Glu Leu Pro Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys
15 20 25
Ala Asp Asp Ser Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn
30 35 40 45
Ile Phe Thr Arg Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly
50 55 60
Asn Gln Asn Arg Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr

65 70 75
 Arg Asp Asn Ala Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys
 80 85 90
 Pro Asp Phe Cys Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr
 95 100 105
 Ile Thr Arg Tyr Phe Tyr Asn Asn Gln Thr Lys His Val Asn Val Ser
 110 115 120 125
 Ser Met Val Asp Ala Trp Ala Ile
 130

<210> 95
 <211> 1307
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..252

<220>
 <221> CDS
 <222> 253..744

<220>
 <221> 3'UTR
 <222> 745..1307

<220>
 <221> polyA_signal
 <222> 1269..1274

<220>
 <221> polyA_site
 <222> 1292..1307

<400> 95
 ctctttgctc taacagacag cagcgacttt aggctggata atagtcaa atcttacctcg 60
 ctctttcact gctagtaaga tcagattgcg tttctttcag ttactcttca atcgccagtt 120
 tcttgatctg cttctaaaag aagaagtaga gaagataaat cctgtcttca atacctggaa 180
 ggaaaaacag aataacctca actccgtttt gaaaaaaaca ttccaagaac tttcatcaga 240
 gattttactt ag atg att tac aca atg aag aaa gta cat gca ctt tgg gct 291
 Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala
 -25 -20 -15
 tct gta tgc ctg ctg ctt aat ctt gcc cct gcc cct ctt aat gct gat 339
 Ser Val Cys Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp
 -10 -5 1
 tct gag gaa gat gaa gaa cac aca att atc aca gat acg gag ttg cca 387
 Ser Glu Glu Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro
 5 10 15
 cca ctg aaa ctt atg cat tca ttt tgt gca ttc aag gcg gat gat ggc 435
 Pro Leu Lys Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly
 20 25 30
 cca tgt aaa gca atc atg aaa aga ttt ttc ttc aat att ttc act cga 483
 Pro Cys Lys Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg
 35 40 45 50
 cag tgc gaa gaa ttt ata tat ggg gga tgt gaa gga aat cag aat cga 531
 Gln Cys Glu Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg
 55 60 65
 ttt gaa agt ctg gaa gag tgc aaa aaa atg tgt aca aga gat aat gca 579
 Phe Glu Ser Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala

```

      70      75      80
aac agg att ata aag aca aca ttg caa caa gaa aag cca gat ttc tgc
Asn Arg Ile Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys      627
      85      90      95
ttt ttg gaa gaa gat cct gga ata tgt cga ggt tat att acc agg tat      675
Phe Leu Glu Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr
      100      105      110
ttt tat aac aat cag aca aaa cag tgt gaa cgt ttc aag tat ggt gga      723
Phe Tyr Asn Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly
      115      120      125      130
tgc ctg ggc aat caa caa ttt tgagacactg gaacaatgca agaacatttg      774
Cys Leu Gly Asn Gln Gln Phe
      135
tgaagatggg ccgaatgggt tccaggtgga taattatgga acccagctca atgctgtgaa      834
taactccctg actccgcaat caaccaaggt tcccagcctt tttgaatttc acgggtccctc      894
atgggtgtctc actccagcag acagaggatt gtgtcgtgcc aatgagaaca gattctacta      954
caattcagtc attgggaaat gccgccatt taagtacagt ggatgtgggg gaaatgaaaa      1014
caattttact tccaacaag aatgtctgag ggcattgtaa aaaggtttca tccaaagaat      1074
atcaaaagga ggcctaatta aaacaaaag aaaaagaaag aagcagagag tgaaaatagc      1134
atatgaagaa atttttgtta aaaatatgtg aatttgttat agcaatgtaa cattaattct      1194
actaaatatt ttatatgaaa tgtttacta tgattttcta tttttcttct aaaatgcttt      1254
taattaatat gttcattaaa ttttctatgc ttattgcaaa aaaaaaaaaa aaa      1307

<210> 96
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> 1..28

<400> 96
Met Ile Tyr Thr Met Lys Lys Val His Ala Leu Trp Ala Ser Val Cys
      -25      -20      -15
Leu Leu Leu Asn Leu Ala Pro Ala Pro Leu Asn Ala Asp Ser Glu Glu
      -10      -5      1
Asp Glu Glu His Thr Ile Ile Thr Asp Thr Glu Leu Pro Pro Leu Lys
5      10      15      20
Leu Met His Ser Phe Cys Ala Phe Lys Ala Asp Asp Gly Pro Cys Lys
      25      30      35
Ala Ile Met Lys Arg Phe Phe Phe Asn Ile Phe Thr Arg Gln Cys Glu
      40      45      50
Glu Phe Ile Tyr Gly Gly Cys Glu Gly Asn Gln Asn Arg Phe Glu Ser
      55      60      65
Leu Glu Glu Cys Lys Lys Met Cys Thr Arg Asp Asn Ala Asn Arg Ile
      70      75      80
Ile Lys Thr Thr Leu Gln Gln Glu Lys Pro Asp Phe Cys Phe Leu Glu
85      90      95      100
Glu Asp Pro Gly Ile Cys Arg Gly Tyr Ile Thr Arg Tyr Phe Tyr Asn
      105      110      115
Asn Gln Thr Lys Gln Cys Glu Arg Phe Lys Tyr Gly Gly Cys Leu Gly
      120      125      130
Asn Gln Gln Phe
      135

<210> 97
<211> 1855
<212> DNA
<213> Homo sapiens

```

<220>
 <221> 5'UTR
 <222> 1..117

<220>
 <221> CDS
 <222> 118..504

<220>
 <221> 3'UTR
 <222> 505..1855

<220>
 <221> polyA_signal
 <222> 1819..1824

<220>
 <221> polyA_site
 <222> 1840..1855

<400> 97
 tccccggccg ccgcccgttgc gctcgccgcg ctcgcaactga agccccgggccc ctgcgcgcgcc 60
 gcggttcgcc ccgcagcctc gccccctgcc caccggggcg gccgtagggc ggtcacg 117
 atg ctg ccg ccc tta ccc tcc cgc ctc ggg ctg ctg ctg ctg ctc 165
 Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu
 -20 -15 -10
 ctg tgc ccg gcg cac gtc ggc gga ctg tgg tgg gct gtg ggc agc ccc 213
 Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
 -5 1 5
 ttg gtt atg gac cct acc agc atc tgc agg aag gca cgg cgg ctg gcc 261
 Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
 10 15 20 25
 ggg cgg cag gcc gag ttg tgc cag gct gag ccg gaa gtg gtg gca gag 309
 Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
 30 35 40
 ctg gct cgg ggc gcc cgg ctc ggg gtg cga gag tgc cag ttc cag ttc 357
 Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
 45 50 55
 cgc ttc cgc cgc tgg aat tgc tcc agc cac agc aag gcc ttt gga cgc 405
 Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
 60 65 70
 atc ctg caa cag ggt cag tgt ggg gag ggg gcg gaa gtg ggg ctg ctt 453
 Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
 75 80 85
 tct ccc tgc tgt ggg acc cga gga gag gag aac tgg ttc gct gaa gtt 501
 Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
 90 95 100 105
 gcc tgagccccac ttccccctca catgtgtctg ggcaccctgc aaggaccctg 554
 Ala
 cctcccaggc ccctggggca gccctccgc cgcagggttc aggtcccagg cccagctga 614
 ccgccccagc ccgcgtgat tgcacctgtc tgcattcaca gacattcggg agacggcctt 674
 cgtgttcgcc atcactgcgg ccggcgccag ccacgccgtc acgcaggcct gttctatggg 734
 cgagctgctg cagtgcggct gccaggcgcc ccgcgggcgg gccccctccc ggccctccgg 794
 cctgcccggc acccccggac cccctggccc cgcgggctcc ccggaaggca gcgccgctg 854
 ggagtgggga ggctgcggcg acgacgtgga ctccggggac gagaagtoga ggctctttat 914
 ggacgcgcgg cacaagcggg gacgcggaga catccgcgcg ttggtgcaac tgcacaacaa 974
 cgaggcgggc aggtctggcg tgcggagcca cacgcgcacc gagtgcaaat gccacgggct 1034
 gtcgggatca tgcgcgctgc gcacctgctg gcagaagctg cctccatttc gcgaggtggg 1094
 cgcgcgggct ctggagcgct tccacggcgc ctcacgcgtc atgggcacca acgacggcaa 1154

```

ggccctgctg cccgccgtcc gcacgctcaa gccgccgggc cgagcggacc tcctctacgc 1214
cgccgattcg cccgacttct gcgcccccaa ccgacgcacc ggctcccccg gcacgcgcgg 1274
tcgcgcctgc aatagcagcg ccccgacct cagcggctgc gacctgctgt gctgcggccg 1334
cgggcaccgc caggagagcg tgcagctcga agagaactgc ctgtgccgct tccactggtg 1394
ctgcgtagta cagtgccacc gctgccgtgt gcgcaaggag ctacagcctct gcctgtgacc 1454
cgccgcccgg ccgctagact gacttcgcgc agcgggtggct cgcacctgtg ggacctcagg 1514
gcaccggcac cgggcgcctc tcgccgctcg agcccagcct ctccctgccca aagcccaact 1574
cccagggctc tggaaatggg gaggcgaggg gcttgagagg aacgcccacc cacgaaggcc 1634
cagggcgcca gacggccccg aaaaggcgt cggggagcgt ttaaaggaca ctgtacaggc 1694
cctccctccc cttggcctct aggaggaaac agtttttttag actggaaaaa agccagtcta 1754
aaggcctctg gatactgggc tccccagaac tgctggccac aggatgggtgg gtgagggttag 1814
tatcaataaa gatatttaaa ccaccaaaaa aaaaaaaaaa a 1855

```

```

<210> 98
<211> 129
<212> PRT
<213> Homo sapiens

```

```

<220>
<221> SIGNAL
<222> 1..24

```

```

<400> 98
Met Leu Pro Pro Leu Pro Ser Arg Leu Gly Leu Leu Leu Leu Leu Leu
      -20      -15      -10
Leu Cys Pro Ala His Val Gly Gly Leu Trp Trp Ala Val Gly Ser Pro
      -5      1      5
Leu Val Met Asp Pro Thr Ser Ile Cys Arg Lys Ala Arg Arg Leu Ala
      10      15      20
Gly Arg Gln Ala Glu Leu Cys Gln Ala Glu Pro Glu Val Val Ala Glu
      25      30      35      40
Leu Ala Arg Gly Ala Arg Leu Gly Val Arg Glu Cys Gln Phe Gln Phe
      45      50      55
Arg Phe Arg Arg Trp Asn Cys Ser Ser His Ser Lys Ala Phe Gly Arg
      60      65      70
Ile Leu Gln Gln Gly Gln Cys Gly Glu Gly Ala Glu Val Gly Leu Leu
      75      80      85
Ser Pro Cys Cys Gly Thr Arg Gly Glu Glu Asn Trp Phe Ala Glu Val
      90      95      100
Ala
105

```

```

<210> 99
<211> 667
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> 5'UTR
<222> 1..94

```

```

<220>
<221> CDS
<222> 95..613

```

```

<220>
<221> 3'UTR
<222> 614..667

```

```

<220>

```


<221> polyA_signal

<222> 636..641

<220>

<221> polyA_site

<222> 652..667

<400> 99

ctctgcaaat ccaggacaca cattgtgctc cgcgctccac taaaggcttg agtgggcaact 60
gttccatctc aacagcccct gttttggaaa ggac atg att gtc aag ggg gtg gcc 115

Met Ile Val Lys Gly Val Ala

1

5

tcc aga act gtg gtt tcc aga ccg ttc ccc ggt aac tgg ctt ttc tct 163
Ser Arg Thr Val Val Ser Arg Pro Phe Pro Gly Asn Trp Leu Phe Ser

10

15

20

tcc atc cag ctg act gat gat cag ggc ccc gtc ctg atg acc act gta 211
Ser Ile Gln Leu Thr Asp Asp Gln Gly Pro Val Leu Met Thr Thr Val

25

30

35

gcc atg cct gtg ttt agt aag cag aac gaa acc aga tcg aag ggc att 259
Ala Met Pro Val Phe Ser Lys Gln Asn Glu Thr Arg Ser Lys Gly Ile

40

45

50

55

ctt ctg gga gtg gtt ggc aca gat gtc cca gtg aaa gaa ctt ctg aag 307
Leu Leu Gly Val Val Gly Thr Asp Val Pro Val Lys Glu Leu Leu Lys

60

65

70

acc atc ccc aaa tac aag tta ggg att cac ggt tat gcc ttt gca atc 355
Thr Ile Pro Lys Tyr Lys Leu Gly Ile His Gly Tyr Ala Phe Ala Ile

75

80

85

aca aat aat gga tat atc ctg acg cat ccg gaa ctc agg ctg ctg tac 403
Thr Asn Asn Gly Tyr Ile Leu Thr His Pro Glu Leu Arg Leu Leu Tyr

90

95

100

gaa gaa gga aaa aag cga agg aaa cct aac tat agt agc gtt gac ctc 451
Glu Glu Gly Lys Lys Arg Arg Lys Pro Asn Tyr Ser Ser Val Asp Leu

105

110

115

tct gag gtg gag tgg gaa gac cga gat gac gtg ttg aga aat gct atg 499
Ser Glu Val Glu Trp Glu Asp Arg Asp Asp Val Leu Arg Asn Ala Met

120

125

130

135

gtg aat cga aag acg ggg aag ttt tcc atg gag gtg aag aag aca gtg 547
Val Asn Arg Lys Thr Gly Lys Phe Ser Met Glu Val Lys Lys Thr Val

140

145

150

gac aaa ggg gta cat ttt tct caa aca ttt ttg ctg ctt aat tta aaa 595
Asp Lys Gly Val His Phe Ser Gln Thr Phe Leu Leu Leu Asn Leu Lys

155

160

165

caa acc act gtg aaa aat tagctttgaa agctatatct ggaataaata 643
Gln Thr Thr Val Lys Asn

170

tctttcgcaa aaaaaaaaaa aaaa 667

<210> 100

<211> 173

<212> PRT

<213> Homo sapiens

<400> 100

Met Ile Val Lys Gly Val Ala Ser Arg Thr Val Val Ser Arg Pro Phe
1 5 10 15

Pro Gly Asn Trp Leu Phe Ser Ser Ile Gln Leu Thr Asp Asp Gln Gly
20 25 30

Pro Val Leu Met Thr Thr Val Ala Met Pro Val Phe Ser Lys Gln Asn
35 40 45

Glu Thr Arg Ser Lys Gly Ile Leu Leu Gly Val Val Gly Thr Asp Val

50 55 60
 Pro Val Lys Glu Leu Leu Lys Thr Ile Pro Lys Tyr Lys Leu Gly Ile
 65 70 75 80
 His Gly Tyr Ala Phe Ala Ile Thr Asn Asn Gly Tyr Ile Leu Thr His
 85 90 95
 Pro Glu Leu Arg Leu Leu Tyr Glu Glu Gly Lys Lys Arg Arg Lys Pro
 100 105 110
 Asn Tyr Ser Ser Val Asp Leu Ser Glu Val Glu Trp Glu Asp Arg Asp
 115 120 125
 Asp Val Leu Arg Asn Ala Met Val Asn Arg Lys Thr Gly Lys Phe Ser
 130 135 140
 Met Glu Val Lys Lys Thr Val Asp Lys Gly Val His Phe Ser Gln Thr
 145 150 155 160
 Phe Leu Leu Leu Asn Leu Lys Gln Thr Thr Val Lys Asn
 165 170

<210> 101
 <211> 1062
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..153

<220>
 <221> CDS
 <222> 154..639

<220>
 <221> 3'UTR
 <222> 640..1062

<220>
 <221> polyA_signal
 <222> 1023..1028

<220>
 <221> polyA_site
 <222> 1047..1062

<400> 101
 attggtgtat ggctttgcag caataactga tggctgtttc ccctcctgct ttatctttca 60
 gttaatgacc agccacggcg tccctgctgt gagctctggc cgctgccttc cagggctccc 120
 gagccacacg ctgggggtgc tggctgaggg aac atg gct tgt tgg cct cag ctg 174
 Met Ala Cys Trp Pro Gln Leu
 1 5
 agg ttg ctg ctg tgg aag aac ctc act ttc aga aga aga caa aca tgt 222
 Arg Leu Leu Leu Trp Lys Asn Leu Thr Phe Arg Arg Arg Gln Thr Cys
 10 15 20
 cag ctg ctg ctg gaa gtg gcc tgg cct cta ttt atc ttc ctg atc ctg 270
 Gln Leu Leu Leu Glu Val Ala Trp Pro Leu Phe Ile Phe Leu Ile Leu
 25 30 35
 atc tct gtt cgg ctg agc tac cca ccc tat gaa caa cat gaa tgc cat 318
 Ile Ser Val Arg Leu Ser Tyr Pro Pro Tyr Glu Gln His Glu Cys His
 40 45 50 55
 ttt cca aat aaa gcc atg ccc tct gca gga aca ctt cct tgg gtt cag 366
 Phe Pro Asn Lys Ala Met Pro Ser Ala Gly Thr Leu Pro Trp Val Gln
 60 65 70
 ggg att atc tgt aat gcc aac aac ccc tgt ttc cgt tac ccg act cct 414

<222> 1..149

<220>

<221> CDS

<222> 150..392

<220>

<221> 3'UTR

<222> 393..933

<220>

<221> polyA_site

<222> 63..933

<400> 103

```
aaaccctcag ggacctggtg tagacgcaga atctgtttca cacaacaact gctatttgaa 60
ggaaaaaaaa aaaaagaagc aaatgatacc aagacaagct cataacagag atccaatcag 120
cagatgtgta cggatgaaaa tacagtggag atg agt cag aaa ccg gcc aag gag 173
                               Met Ser Gln Lys Pro Ala Lys Glu
                               1                               5
ggt ccc aga ctc tcc aaa aac cag aag tac tcc gaa cac ttc agc ata 221
Gly Pro Arg Leu Ser Lys Asn Gln Lys Tyr Ser Glu His Phe Ser Ile
10                               15                               20
cac tgc tgc ccg ccg ttc acc ttc ctc aat tcc aag aag gag ata gtg 269
His Cys Cys Pro Pro Phe Thr Phe Leu Asn Ser Lys Lys Glu Ile Val
25                               30                               35                               40
gat cgg aaa tac agc atc tgt aag agc ggc tgc ttc tac cag aag aaa 317
Asp Arg Lys Tyr Ser Ile Cys Lys Ser Gly Cys Phe Tyr Gln Lys Lys
45                               50                               55
gag gag gac tgg atc tgc tgc gcc tgc cag aag acc aga ttg aaa agg 365
Glu Glu Asp Trp Ile Cys Cys Ala Cys Gln Lys Thr Arg Leu Lys Arg
60                               65                               70
aag atc agg cca acc cca aag aag aag tgaccaagga ggagtttaaa 412
Lys Ile Arg Pro Thr Pro Lys Lys Lys
75                               80
ytgaatgaac aacctcggtc cctggactca ttgcttcaca acccatctac ccctggatga 472
agttatctgg cttcaaatat tatgcagggg caaacacctg ctgatgtggc aactgctgat 532
gctcatgggc cccatggcat gggggcctca gggcagcctg cctggagtac tttgaagatg 592
tcatccatt gtcttctgac ctctataatt gccactgaga gatctgctgt cagtctgctt 652
atccttccac ggactcaagt ttcttcaatc tgaagataca tgtctttctc caaggacatg 712
tggaaaaaaa aaagatgtta tacaaccatc aaagtggcaa aaataaaaaa aattggctgg 772
gcgtggtggc gggcgctgt ggtcccagct actcgggagg ctgaggcagg agaatggcgt 832
gaacctggga ggcggagctt gcagtgagcc gagatgcac cactgcactc cagcctgggc 892
gacagagcga gactctgtct caaacaaaaa aaaaaaaaaa a 933
```

<210> 104

<211> 81

<212> PRT

<213> Homo sapiens

<400> 104

```
Met Ser Gln Lys Pro Ala Lys Glu Gly Pro Arg Leu Ser Lys Asn Gln
1                               5                               10                               15
Lys Tyr Ser Glu His Phe Ser Ile His Cys Cys Pro Pro Phe Thr Phe
20                               25                               30
Leu Asn Ser Lys Lys Glu Ile Val Asp Arg Lys Tyr Ser Ile Cys Lys
35                               40                               45
Ser Gly Cys Phe Tyr Gln Lys Lys Glu Glu Asp Trp Ile Cys Cys Ala
50                               55                               60
Cys Gln Lys Thr Arg Leu Lys Arg Lys Ile Arg Pro Thr Pro Lys Lys
```

65
Lys

70

75

80

<210> 105
<211> 1187
<212> DNA
<213> Homo sapiens

<220>
<221> 5'UTR
<222> 1..34

<220>
<221> CDS
<222> 35..1069

<220>
<221> 3'UTR
<222> 1070..1187

<220>
<221> polyA_signal
<222> 1146..1151

<220>
<221> polyA_site
<222> 1172..1187

<400> 105
accactttgg tagtgccagt gtgactcatc caca atg att tct cca gtg ctc atc 55
Met Ile Ser Pro Val Leu Ile
-15
ttg ttc tcg agt ttt ctc tgc cat gtt gct att gca gga cgg acc tgt 103
Leu Phe Ser Ser Phe Leu Cys His Val Ala Ile Ala Gly Arg Thr Cys
-10 -5 1 5
ccc aag cca gat gat tta cca ttt tcc aca gtg gtc ccg tta aaa aca 151
Pro Lys Pro Asp Asp Leu Pro Phe Ser Thr Val Val Pro Leu Lys Thr
10 15 20
ttc tat gag cca gga gaa gag att acg tat tcc tgc aag ccg ggc tat 199
Phe Tyr Glu Pro Gly Glu Glu Ile Thr Tyr Ser Cys Lys Pro Gly Tyr
25 30 35
gtg tcc cga gga ggg atg aga aag ttt atc tgc cct ctc aca gga ctg 247
Val Ser Arg Gly Gly Met Arg Lys Phe Ile Cys Pro Leu Thr Gly Leu
40 45 50
tgg ctc atc aac act ctg aaa tgt aca ccc aga gta tgt cct ttt gct 295
Trp Leu Ile Asn Thr Leu Lys Cys Thr Pro Arg Val Cys Pro Phe Ala
55 60 65
gga atc tta gaa aat gga gcc gta cgc tat acg act ttt gaa tat ccc 343
Gly Ile Leu Glu Asn Gly Ala Val Arg Tyr Thr Thr Phe Glu Tyr Pro
70 75 80 85
aac acg atc agt ttt tct tgt aac act ggg ttt tat ctg aat ggc gct 391
Asn Thr Ile Ser Phe Ser Cys Asn Thr Gly Phe Tyr Leu Asn Gly Ala
90 95 100
gat tct gcc aag tgc act gag gaa gga aaa tgg agc ccg gag ctt cct 439
Asp Ser Ala Lys Cys Thr Glu Glu Gly Lys Trp Ser Pro Glu Leu Pro
105 110 115
gtc tgt gct ccc atc atc tgc cct cca cca tcc ata cct acg ttt gca 487
Val Cys Ala Pro Ile Ile Cys Pro Pro Pro Ser Ile Pro Thr Phe Ala
120 125 130
aca ctt cgt gtt tat aag cca tca gct gga aac aat tcc ctc tat cgg 535

Thr	Leu	Arg	Val	Tyr	Lys	Pro	Ser	Ala	Gly	Asn	Asn	Ser	Leu	Tyr	Arg	
135						140					145					
gac	aca	gca	gtt	ttt	gaa	tgt	ttg	cca	caa	cat	gcg	atg	ttt	gga	aat	583
Asp	Thr	Ala	Val	Phe	Glu	Cys	Leu	Pro	Gln	His	Ala	Met	Phe	Gly	Asn	
150					155					160					165	
gat	aca	att	acc	tgc	acg	aca	cat	gga	aat	tgg	act	aaa	tta	cca	gaa	631
Asp	Thr	Ile	Thr	Cys	Thr	Thr	His	Gly	Asn	Trp	Thr	Lys	Leu	Pro	Glu	
				170					175						180	
tgc	agg	gaa	gta	aaa	tgc	cca	ttc	cca	tca	aga	cca	gac	aat	gga	ttt	679
Cys	Arg	Glu	Val	Lys	Cys	Pro	Phe	Pro	Ser	Arg	Pro	Asp	Asn	Gly	Phe	
			185					190					195			
gtg	aac	tat	cct	gca	aaa	cca	aca	ctt	tat	tac	aag	gat	aaa	gcc	aca	727
Val	Asn	Tyr	Pro	Ala	Lys	Pro	Thr	Leu	Tyr	Tyr	Lys	Asp	Lys	Ala	Thr	
	200						205					210				
ttt	ggc	tgc	cat	gat	gga	tat	tct	ctg	gat	ggc	ccg	gaa	gaa	ata	gaa	775
Phe	Gly	Cys	His	Asp	Gly	Tyr	Ser	Leu	Asp	Gly	Pro	Glu	Glu	Ile	Glu	
	215				220					225						
tgt	acc	aaa	ctg	gga	aac	tgg	tct	gcc	atg	cca	agt	tgt	aaa	gca	tct	823
Cys	Thr	Lys	Leu	Gly	Asn	Trp	Ser	Ala	Met	Pro	Ser	Cys	Lys	Ala	Ser	
230					235				240						245	
tgt	aaa	gta	cct	gtg	aaa	aaa	gcc	act	gtg	gtg	tac	caa	gga	gag	aga	871
Cys	Lys	Val	Pro	Val	Lys	Lys	Ala	Thr	Val	Val	Tyr	Gln	Gly	Glu	Arg	
			250					255						260		
gta	aag	att	cag	gaa	aaa	ttt	aag	aat	gga	atg	cta	cat	ggt	gat	aaa	919
Val	Lys	Ile	Gln	Glu	Lys	Phe	Lys	Asn	Gly	Met	Leu	His	Gly	Asp	Lys	
			265					270					275			
gtt	tct	ttc	ttc	tgc	aaa	aat	aag	gaa	aag	aag	tgt	agc	tat	aca	gag	967
Val	Ser	Phe	Phe	Cys	Lys	Asn	Lys	Glu	Lys	Lys	Cys	Ser	Tyr	Thr	Glu	
	280						285				290					
gat	gct	cag	tgt	ata	gat	ggc	act	atc	gaa	gtc	ccc	aaa	tgc	ttc	aag	1015
Asp	Ala	Gln	Cys	Ile	Asp	Gly	Thr	Ile	Glu	Val	Pro	Lys	Cys	Phe	Lys	
	295					300					305					
gaa	cac	agt	tct	ctg	gct	ttt	tgg	aaa	act	gat	gca	tcc	gat	gta	aag	1063
Glu	His	Ser	Ser	Leu	Ala	Phe	Trp	Lys	Thr	Asp	Ala	Ser	Asp	Val	Lys	
310					315					320					325	
cca	tgc	taaggtggtt	ttcagattcc	acataaaatg	tcacacttgt	ttcttgttca										1119
Pro	Cys															
tc	caaggaac	ctaattgaaa	tttaaaaata	aagctactga	atttattgcc	gcaaaaaaaaa										1179
aaaaaaaa																1187

<210> 106

<211> 345

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> 1..19

<400> 106

Met	Ile	Ser	Pro	Val	Leu	Ile	Leu	Phe	Ser	Ser	Phe	Leu	Cys	His	Val	
				-15					-10					-5		
Ala	Ile	Ala	Gly	Arg	Thr	Cys	Pro	Lys	Pro	Asp	Asp	Leu	Pro	Phe	Ser	
		1					5					10				
Thr	Val	Val	Pro	Leu	Lys	Thr	Phe	Tyr	Glu	Pro	Gly	Glu	Glu	Ile	Thr	
	15					20					25					
Tyr	Ser	Cys	Lys	Pro	Gly	Tyr	Val	Ser	Arg	Gly	Gly	Met	Arg	Lys	Phe	
	30				35					40					45	
Ile	Cys	Pro	Leu	Thr	Gly	Leu	Trp	Leu	Ile	Asn	Thr	Leu	Lys	Cys	Thr	
				50					55						60	

Pro	Arg	Val	Cys	Pro	Phe	Ala	Gly	Ile	Leu	Glu	Asn	Gly	Ala	Val	Arg
			65					70					75		
Tyr	Thr	Thr	Phe	Glu	Tyr	Pro	Asn	Thr	Ile	Ser	Phe	Ser	Cys	Asn	Thr
		80					85					90			
Gly	Phe	Tyr	Leu	Asn	Gly	Ala	Asp	Ser	Ala	Lys	Cys	Thr	Glu	Glu	Gly
	95				100					105					
Lys	Trp	Ser	Pro	Glu	Leu	Pro	Val	Cys	Ala	Pro	Ile	Ile	Cys	Pro	Pro
110					115					120					125
Pro	Ser	Ile	Pro	Thr	Phe	Ala	Thr	Leu	Arg	Val	Tyr	Lys	Pro	Ser	Ala
				130					135					140	
Gly	Asn	Asn	Ser	Leu	Tyr	Arg	Asp	Thr	Ala	Val	Phe	Glu	Cys	Leu	Pro
			145					150					155		
Gln	His	Ala	Met	Phe	Gly	Asn	Asp	Thr	Ile	Thr	Cys	Thr	Thr	His	Gly
		160				165						170			
Asn	Trp	Thr	Lys	Leu	Pro	Glu	Cys	Arg	Glu	Val	Lys	Cys	Pro	Phe	Pro
	175				180						185				
Ser	Arg	Pro	Asp	Asn	Gly	Phe	Val	Asn	Tyr	Pro	Ala	Lys	Pro	Thr	Leu
190					195					200					205
Tyr	Tyr	Lys	Asp	Lys	Ala	Thr	Phe	Gly	Cys	His	Asp	Gly	Tyr	Ser	Leu
			210					215						220	
Asp	Gly	Pro	Glu	Glu	Ile	Glu	Cys	Thr	Lys	Leu	Gly	Asn	Trp	Ser	Ala
		225						230					235		
Met	Pro	Ser	Cys	Lys	Ala	Ser	Cys	Lys	Val	Pro	Val	Lys	Lys	Ala	Thr
		240					245					250			
Val	Val	Tyr	Gln	Gly	Glu	Arg	Val	Lys	Ile	Gln	Glu	Lys	Phe	Lys	Asn
	255					260					265				
Gly	Met	Leu	His	Gly	Asp	Lys	Val	Ser	Phe	Phe	Cys	Lys	Asn	Lys	Glu
270					275					280					285
Lys	Lys	Cys	Ser	Tyr	Thr	Glu	Asp	Ala	Gln	Cys	Ile	Asp	Gly	Thr	Ile
			290					295						300	
Glu	Val	Pro	Lys	Cys	Phe	Lys	Glu	His	Ser	Ser	Leu	Ala	Phe	Trp	Lys
		305						310					315		
Thr	Asp	Ala	Ser	Asp	Val	Lys	Pro	Cys							
		320					325								

<210> 107
 <211> 1520
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..15

<220>
 <221> CDS
 <222> 16..1449

<220>
 <221> 3'UTR
 <222> 1450..1520

<220>
 <221> polyA_signal
 <222> 1483..1488

<220>
 <221> polyA_site
 <222> 1505..1520

<400> 107

```

cttttttttg acaag atg gcg gca gga ggc agt ggc gtt ggt ggg aag cgc      51
      Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg
          1          5          10
agc tcg aaa agc gat gcc gat tct ggt ttc ctg ggg ctg cgg ccc act      99
Ser Ser Lys Ser Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr
          15          20          25
tcg gtg gac cca gcg ctg agg cgg cgg cgg cga ggc cca aga aat aag      147
Ser Val Asp Pro Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys
          30          35          40
aag cgg ggc tgg cgg cgg ctt gct cag gag ccg ctg ggg ctg gag gtt      195
Lys Arg Gly Trp Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val
          45          50          55          60
gac cag ttc ctg gaa gac gtg cgg cta cag gag cgc acg agc ggt ggc      243
Asp Gln Phe Leu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly
          65          70          75
ttg ttg tca gag gcc cca aat gaa aaa ctc ttc ttc gtg gac act ggc      291
Leu Leu Ser Glu Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly
          80          85          90
tcc aag gaa aaa ggg ctg aca aag aag aga acc aaa gtc cag aag aag      339
Ser Lys Glu Lys Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys
          95          100          105
tca ctg ctt ctc aag aaa ccc ctt cgg gtt gac ctc atc ctc gag aac      387
Ser Leu Leu Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn
          110          115          120
aca tcc aaa gtc cct gcc ccc aaa gac gtc ctc gcc cac cag gtc ccc      435
Thr Ser Lys Val Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro
          125          130          135          140
aac gcc aag aag ctc agg cgg aag gag cag cta tgg gag aag ctg gcc      483
Asn Ala Lys Lys Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala
          145          150          155
aag cag ggc gag ctg ccc cgg gag gtg cgc agg gcc cag gcc cgg ctc      531
Lys Gln Gly Glu Leu Pro Arg Glu Val Arg Arg Ala Gln Ala Arg Leu
          160          165          170
ctc aac cct tct gca aca agg gcc aag ccc ggg ccc cag gac acc gta      579
Leu Asn Pro Ser Ala Thr Arg Ala Lys Pro Gly Pro Gln Asp Thr Val
          175          180          185
gag cgg ccc ttc tac gac ctc tgg gcc tca gac aac ccc ctg gac agg      627
Glu Arg Pro Phe Tyr Asp Leu Trp Ala Ser Asp Asn Pro Leu Asp Arg
          190          195          200
ccg ttg gtt ggc cag gat gag ttt ttc ctg gag cag acc aag aag aaa      675
Pro Leu Val Gly Gln Asp Glu Phe Phe Leu Gln Thr Lys Lys Lys
          205          210          215          220
gga gtg aag cgg cca gca cgc ctg cac acc aag ccg tcc cag gca ccc      723
Gly Val Lys Arg Pro Ala Arg Leu His Thr Lys Pro Ser Gln Ala Pro
          225          230          235
gcc gtg gag gtg gcg cct gcc gga gct tcc tac aat cca tcc ttt gaa      771
Ala Val Glu Val Ala Pro Ala Gly Ala Ser Tyr Asn Pro Ser Phe Glu
          240          245          250
gac cac cag acc ctg ctc tca gcg gcc cac gag gtg gag ttg cag cgg      819
Asp His Gln Thr Leu Leu Ser Ala Ala His Glu Val Glu Leu Gln Arg
          255          260          265
cag aag gag gcg gag aag ctg gag cgg cag ctg gcc ctg ccc gcc acg      867
Gln Lys Glu Ala Glu Lys Leu Glu Arg Gln Leu Ala Leu Pro Ala Thr
          270          275          280
gag cag gcc gcc acc cag gag tcc aca ttc cag gag ctg tgc gag ggg      915
Glu Gln Ala Ala Thr Gln Glu Ser Thr Phe Gln Glu Leu Cys Glu Gly
          285          290          295          300
ctg ctg gag gag tcg gat ggt gag ggg gag cca ggc cag ggc gag ggg      963
Leu Leu Glu Glu Ser Asp Gly Glu Gly Glu Pro Gly Gln Gly Glu Gly

```


	305	310	315	
ccg gag gct ggg gat gcc gag gtc tgt ccc acg ccc gcc cgc ctg gcc				1011
Pro Glu Ala Gly Asp Ala Glu Val Cys Pro Thr Pro Ala Arg Leu Ala				
	320	325	330	
acc aca gag aag aag acg gag cag cag cgg cgg cgg gag aag gct gtg				1059
Thr Thr Glu Lys Lys Thr Glu Gln Gln Arg Arg Arg Glu Lys Ala Val				
	335	340	345	
cac agg ctg cgg gta cag cag gcc gcg ttg cgg gcc gcc cgg ctc cgg				1107
His Arg Leu Arg Val Gln Gln Ala Ala Leu Arg Ala Ala Arg Leu Arg				
	350	355	360	
cac cag gag ctg ttc cgg ctg cgc ggg atc aag gcc cag gtg gcc ctg				1155
His Gln Glu Leu Phe Arg Leu Arg Gly Ile Lys Ala Gln Val Ala Leu				
	365	370	375	380
agg ctg gcg gag ctg gcg cgg cgg cag agg cgg cgg cag gcg cgg cgg				1203
Arg Leu Ala Glu Leu Ala Arg Arg Gln Arg Arg Arg Gln Ala Arg Arg				
	385	390	395	
gag gct gag gct gac aag ccc cga agg ctg ggg cgg ctc aag tac cag				1251
Glu Ala Glu Ala Asp Lys Pro Arg Arg Leu Gly Arg Leu Lys Tyr Gln				
	400	405	410	
gca cct gac atc gac gtg cag ctg agc tcg gag ctg aca gac tcg ctc				1299
Ala Pro Asp Ile Asp Val Gln Leu Ser Ser Glu Leu Thr Asp Ser Leu				
	415	420	425	
agg acc ctg aag ccc gag gcc aac atc ctt cga gac cgg ttc aag agc				1347
Arg Thr Leu Lys Pro Glu Gly Asn Ile Leu Arg Asp Arg Phe Lys Ser				
	430	435	440	
ttc cag agg agg aat atg atc gag cct cga gag aga gcc aag ttc aaa				1395
Phe Gln Arg Arg Asn Met Ile Glu Pro Arg Glu Arg Ala Lys Phe Lys				
	445	450	455	460
cgc aag tac aag gtg aag ctg gtg gag aag cgg gcg ttc cgt gag atc				1443
Arg Lys Tyr Lys Val Lys Leu Val Glu Lys Arg Ala Phe Arg Glu Ile				
	465	470	475	
cag ttg tagctgccat cagatgccgg agactcgccc ttcaataaaa aatctcttct				1499
Gln Leu				
agctcaaaaa aaaaaaaaaa a				1520

<210> 108
 <211> 478
 <212> PRT
 <213> Homo sapiens

<400> 108
 Met Ala Ala Gly Gly Ser Gly Val Gly Gly Lys Arg Ser Ser Lys Ser
 1 5 10 15
 Asp Ala Asp Ser Gly Phe Leu Gly Leu Arg Pro Thr Ser Val Asp Pro
 20 25 30
 Ala Leu Arg Arg Arg Arg Arg Gly Pro Arg Asn Lys Lys Arg Gly Trp
 35 40 45
 Arg Arg Leu Ala Gln Glu Pro Leu Gly Leu Glu Val Asp Gln Phe Leu
 50 55 60
 Glu Asp Val Arg Leu Gln Glu Arg Thr Ser Gly Gly Leu Leu Ser Glu
 65 70 75 80
 Ala Pro Asn Glu Lys Leu Phe Phe Val Asp Thr Gly Ser Lys Glu Lys
 85 90 95
 Gly Leu Thr Lys Lys Arg Thr Lys Val Gln Lys Lys Ser Leu Leu Leu
 100 105 110
 Lys Lys Pro Leu Arg Val Asp Leu Ile Leu Glu Asn Thr Ser Lys Val
 115 120 125
 Pro Ala Pro Lys Asp Val Leu Ala His Gln Val Pro Asn Ala Lys Lys
 130 135 140
 Leu Arg Arg Lys Glu Gln Leu Trp Glu Lys Leu Ala Lys Gln Gly Glu

145		150		155		160									
Leu	Pro	Arg	Glu	Val	Arg	Arg	Ala	Gln	Ala	Arg	Leu	Leu	Asn	Pro	Ser
		165		170		175									
Ala	Thr	Arg	Ala	Lys	Pro	Gly	Pro	Gln	Asp	Thr	Val	Glu	Arg	Pro	Phe
		180		185		190									
Tyr	Asp	Leu	Trp	Ala	Ser	Asp	Asn	Pro	Leu	Asp	Arg	Pro	Leu	Val	Gly
		195		200		205									
Gln	Asp	Glu	Phe	Phe	Leu	Glu	Gln	Thr	Lys	Lys	Lys	Gly	Val	Lys	Arg
		210		215		220									
Pro	Ala	Arg	Leu	His	Thr	Lys	Pro	Ser	Gln	Ala	Pro	Ala	Val	Glu	Val
225				230		235									240
Ala	Pro	Ala	Gly	Ala	Ser	Tyr	Asn	Pro	Ser	Phe	Glu	Asp	His	Gln	Thr
				245		250								255	
Leu	Leu	Ser	Ala	Ala	His	Glu	Val	Glu	Leu	Gln	Arg	Gln	Lys	Glu	Ala
			260			265							270		
Glu	Lys	Leu	Glu	Arg	Gln	Leu	Ala	Leu	Pro	Ala	Thr	Glu	Gln	Ala	Ala
		275				280							285		
Thr	Gln	Glu	Ser	Thr	Phe	Gln	Glu	Leu	Cys	Glu	Gly	Leu	Leu	Glu	Glu
		290				295					300				
Ser	Asp	Gly	Glu	Gly	Glu	Pro	Gly	Gln	Gly	Glu	Gly	Pro	Glu	Ala	Gly
305					310				315						320
Asp	Ala	Glu	Val	Cys	Pro	Thr	Pro	Ala	Arg	Leu	Ala	Thr	Thr	Glu	Lys
				325		330								335	
Lys	Thr	Glu	Gln	Arg	Arg	Arg	Glu	Lys	Ala	Val	His	Arg	Leu	Arg	
			340			345						350			
Val	Gln	Gln	Ala	Ala	Leu	Arg	Ala	Ala	Arg	Leu	Arg	His	Gln	Glu	Leu
		355				360						365			
Phe	Arg	Leu	Arg	Gly	Ile	Lys	Ala	Gln	Val	Ala	Leu	Arg	Leu	Ala	Glu
		370				375					380				
Leu	Ala	Arg	Arg	Gln	Arg	Arg	Arg	Gln	Ala	Arg	Arg	Glu	Ala	Glu	Ala
385				390					395						400
Asp	Lys	Pro	Arg	Arg	Leu	Gly	Arg	Leu	Lys	Tyr	Gln	Ala	Pro	Asp	Ile
			405					410						415	
Asp	Val	Gln	Leu	Ser	Ser	Glu	Leu	Thr	Asp	Ser	Leu	Arg	Thr	Leu	Lys
			420					425					430		
Pro	Glu	Gly	Asn	Ile	Leu	Arg	Asp	Arg	Phe	Lys	Ser	Phe	Gln	Arg	Arg
		435				440						445			
Asn	Met	Ile	Glu	Pro	Arg	Glu	Arg	Ala	Lys	Phe	Lys	Arg	Lys	Tyr	Lys
		450				455					460				
Val	Lys	Leu	Val	Glu	Lys	Arg	Ala	Phe	Arg	Glu	Ile	Gln	Leu		
465					470					475					

<210> 109
 <211> 1789
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..94

<220>
 <221> CDS
 <222> 95..1252

<220>
 <221> 3'UTR
 <222> 1253..1789

<220>

<221> polyA_signal
<222> 1751..1756

<220>
<221> polyA_site
<222> 1774..1789

<400> 109
 ggtcttgcaa tatttattct gctttcgggt agatgggagg cccggggacc tggctggggt 60
 tctgccaagc ttctccgata cccaggtttc ataa atg tgt ttg ttg ctt tcc tgc 115
 Met Cys Leu Leu Leu Ser Cys
 -10
 cct tgc cac ccc tct gcc cac gga cag tcc atg tgg att gag aga acc 163
 Pro Cys His Pro Ser Ala His Gly Gln Ser Met Trp Ile Glu Arg Thr
 -5 1 5
 tcc ttc gtg act gca tac aag ctg ccg ggg atc ctg cgc tgg ttt gag 211
 Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp Phe Glu
 10 15 20 25
 gtg gtg cac atg tgc cag acc aca att agt cct ctg gag aat gcc ata 259
 Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn Ala Ile
 30 35 40
 gaa acc atg tcc acg gcc aat gag aag atc ctg atg atg ata aac cag 307
 Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu Met Met Ile Asn Gln
 45 50 55
 tac cag agt gat gag acc ctc ccc atc aac cca ctc tcc atg ctc ctg 355
 Tyr Gln Ser Asp Glu Thr Leu Pro Ile Asn Pro Leu Ser Met Leu Leu
 60 65 70
 aac ggg att gtg gac cct gct gtc atg gga ggc ttc gcc aag tat gag 403
 Asn Gly Ile Val Asp Pro Ala Val Met Gly Gly Phe Ala Lys Tyr Glu
 75 80 85
 aag gcc ttc ttc act gaa gag tat gtc agg gac cac cct gag gac cag 451
 Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg Asp His Pro Glu Asp Gln
 90 95 100 105
 gac aag ctg acc cac ctc aag gac ctg att gca tgg cag atc ccc ttc 499
 Asp Lys Leu Thr His Leu Lys Asp Leu Ile Ala Trp Gln Ile Pro Phe
 110 115 120
 ttg gga gct ggg att aag atc cat gag aaa agg gtg tca gat aac ttg 547
 Leu Gly Ala Gly Ile Lys Ile His Glu Lys Arg Val Ser Asp Asn Leu
 125 130 135
 cga ccc ttc cat gac cgg atg gag gaa tgt ttc aag aac ctg aaa atg 595
 Arg Pro Phe His Asp Arg Met Glu Glu Cys Phe Lys Asn Leu Lys Met
 140 145 150
 aag gtg gag aag gag tac ggt gtc cga gag atg cct gac ttt gac gac 643
 Lys Val Glu Lys Glu Tyr Gly Val Arg Glu Met Pro Asp Phe Asp Asp
 155 160 165
 agg aga gtg ggc cgt ccc agg tct atg ctg cgc tca tac aga cag atg 691
 Arg Arg Val Gly Arg Pro Arg Ser Met Leu Arg Ser Tyr Arg Gln Met
 170 175 180 185
 tcc atc atc tct ctg gct tcc atg aat tct gac tgc agc acc ccc agc 739
 Ser Ile Ile Ser Leu Ala Ser Met Asn Ser Asp Cys Ser Thr Pro Ser
 190 195 200
 aag cct acc tca gag agc ttt gac ctg gaa tta gca tca ccc aag acg 787
 Lys Pro Thr Ser Glu Ser Phe Asp Leu Glu Leu Ala Ser Pro Lys Thr
 205 210 215
 ccg aga gtg gag cag gag gaa ccg atc tcc ccg ggg agc acc ctg cct 835
 Pro Arg Val Glu Gln Glu Glu Pro Ile Ser Pro Gly Ser Thr Leu Pro
 220 225 230
 gag gtc aag ctg cgg agg tcc aag aag agg aca aag aga agc agc gta 883
 Glu Val Lys Leu Arg Arg Ser Lys Lys Arg Thr Lys Arg Ser Ser Val
 235 240 245

```

gtt ttt gcg gat gag aaa gca gct gca gag tcg gac ctg aag cgg ctt 931
Val Phe Ala Asp Glu Lys Ala Ala Ala Glu Ser Asp Leu Lys Arg Leu
250 255 260 265
tcc agg aag cat gag ttc atg agt gac acc aac ctc tcg gag cat gcg 979
Ser Arg Lys His Glu Phe Met Ser Asp Thr Asn Leu Ser Glu His Ala
270 275 280
gcc atc ccc ctc aag gcg tct gtc ctc tct caa atg agc ttt gcc agc 1027
Ala Ile Pro Leu Lys Ala Ser Val Leu Ser Gln Met Ser Phe Ala Ser
285 290 295
cag tcc atg cct acc atc cca gcc ctg gcg ctc tca gtg gca ggc atc 1075
Gln Ser Met Pro Thr Ile Pro Ala Leu Ala Leu Ser Val Ala Gly Ile
300 305 310
cct ggg ttg gat gag gcc aac aca tct ccc cgc ctc agc cag acc ttc 1123
Pro Gly Leu Asp Glu Ala Asn Thr Ser Pro Arg Leu Ser Gln Thr Phe
315 320 325
ctc caa ctc tca gat ggt gac aag aag aca ctc aca cgg aag aag gtc 1171
Leu Gln Leu Ser Asp Gly Asp Lys Lys Thr Leu Thr Arg Lys Lys Val
330 335 340 345
aat cag ttc ttc aag aca atg ctg gcc agc aaa tcg gct gaa gaa ggc 1219
Asn Gln Phe Phe Lys Thr Met Leu Ala Ser Lys Ser Ala Glu Glu Gly
350 355 360
aaa cag atc cca gac tcg ctg tcc acg gac ctg tgagctgctg ctgactaggg 1272
Lys Gln Ile Pro Asp Ser Leu Ser Thr Asp Leu
365 370
ctgcatggga gagccagggga ggggagtttc tggaagagga aagccatgcg tggaacatcg 1332
aagcctcaga gagggggaga ctgtccccat cagttgtcct tacttagagg agacagagag 1392
gccaatcagg tcccagagct tgaatgctaa caagcccagc atcccctggg gctgtgatca 1452
tggtggatga ggaagcctca acgtagattc ctgaactcaa ggtaccagca agaatgcctt 1512
ctcccagtg gctctcccca acatcctagg cacagctttc ataaccagc ttcttaggtg 1572
taagaaactg tttttatctc atttattaag tctcagaact taacagaaaa ggaagccttt 1632
taaataattct ttttaatttt attttagatt aacagttttg tactttacat tttttatac 1692
aaccaaccag tttcttttct agccaatcat ctctgaagag ttgctgtttc ttactgacaa 1752
taaaaaatgt tctcttggtt caaaaaaaaa aaaaaaa 1789

```

<210> 110
 <211> 386
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> 1..15

```

<400> 110
Met Cys Leu Leu Leu Ser Cys Pro Cys His Pro Ser Ala His Gly Gln
-15 -10 -5 1
Ser Met Trp Ile Glu Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro
5 10 15
Gly Ile Leu Arg Trp Phe Glu Val Val His Met Ser Gln Thr Thr Ile
20 25 30
Ser Pro Leu Glu Asn Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys
35 40 45
Ile Leu Met Met Ile Asn Gln Tyr Gln Ser Asp Glu Thr Leu Pro Ile
50 55 60 65
Asn Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met
70 75 80
Gly Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val
85 90 95
Arg Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu
100 105 110

```

Ile Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys Ile His Glu
 115 120 125
 Lys Arg Val Ser Asp Asn Leu Arg Pro Phe His Asp Arg Met Glu Glu
 130 135 140 145
 Cys Phe Lys Asn Leu Lys Met Lys Val Glu Lys Glu Tyr Gly Val Arg
 150 155 160
 Glu Met Pro Asp Phe Asp Asp Arg Arg Val Gly Arg Pro Arg Ser Met
 165 170 175
 Leu Arg Ser Tyr Arg Gln Met Ser Ile Ile Ser Leu Ala Ser Met Asn
 180 185 190
 Ser Asp Cys Ser Thr Pro Ser Lys Pro Thr Ser Glu Ser Phe Asp Leu
 195 200 205
 Glu Leu Ala Ser Pro Lys Thr Pro Arg Val Glu Gln Glu Glu Pro Ile
 210 215 220 225
 Ser Pro Gly Ser Thr Leu Pro Glu Val Lys Leu Arg Arg Ser Lys Lys
 230 235 240
 Arg Thr Lys Arg Ser Ser Val Val Phe Ala Asp Glu Lys Ala Ala Ala
 245 250 255
 Glu Ser Asp Leu Lys Arg Leu Ser Arg Lys His Glu Phe Met Ser Asp
 260 265 270
 Thr Asn Leu Ser Glu His Ala Ala Ile Pro Leu Lys Ala Ser Val Leu
 275 280 285
 Ser Gln Met Ser Phe Ala Ser Gln Ser Met Pro Thr Ile Pro Ala Leu
 290 295 300 305
 Ala Leu Ser Val Ala Gly Ile Pro Gly Leu Asp Glu Ala Asn Thr Ser
 310 315 320
 Pro Arg Leu Ser Gln Thr Phe Leu Gln Leu Ser Asp Gly Asp Lys Lys
 325 330 335
 Thr Leu Thr Arg Lys Lys Val Asn Gln Phe Phe Lys Thr Met Leu Ala
 340 345 350
 Ser Lys Ser Ala Glu Glu Gly Lys Gln Ile Pro Asp Ser Leu Ser Thr
 355 360 365
 Asp Leu
 370

<210> 111
 <211> 1408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> 5'UTR
 <222> 1..102

<220>
 <221> CDS
 <222> 103..1263

<220>
 <221> 3'UTR
 <222> 1264..1408

<220>
 <221> polyA_signal
 <222> 1341..1346

<220>
 <221> polyA_site
 <222> 1365..1408

<400> 111
cttcttgact ctctgttcac agaactcagg ctgcctccag ccagcctttg cccgctagac 60
tcactggccc tgatcacttg aaggtgcagc aagtcactga ga atg agc act ttc 114
Met Ser Thr Phe
1
ttc tcg gac aca gca tgg atc tgc ctg gct gtc ccc aca gta cta tgt 162
Phe Ser Asp Thr Ala Trp Ile Cys Leu Ala Val Pro Thr Val Leu Cys
5 10 15 20
ggg aca gta ttt tgc aaa tac aag aag agc tca ggg cag ctg tgg agc 210
Gly Thr Val Phe Cys Lys Tyr Lys Lys Ser Ser Gly Gln Leu Trp Ser
25 30 35
tgg atg gtc tgc ctg gca ggc ctc tgt gca gtc tgc ctg ctc atc ctg 258
Trp Met Val Cys Leu Ala Gly Leu Cys Ala Val Cys Leu Leu Ile Leu
40 45 50
tcc cct ttt tgg ggc ttg atc ctc ttc tcg gtg tca tgc ttc ctc atg 306
Ser Pro Phe Trp Gly Leu Ile Leu Phe Ser Val Ser Cys Phe Leu Met
55 60 65
tat act tac tta tct ggc caa gaa ttg tta cct gtg gat cag aag gca 354
Tyr Thr Tyr Leu Ser Gly Gln Glu Leu Leu Pro Val Asp Gln Lys Ala
70 75 80
gtc ctg gtg aca ggt ggt gat tgc ggg ctt ggc cat gct ttg tgc aag 402
Val Leu Val Thr Gly Gly Asp Cys Gly Leu Gly His Ala Leu Cys Lys
85 90 95 100
tat ctg gat gag ctg ggc ttc acg gta ttt gcc gga gtt ttg aat gaa 450
Tyr Leu Asp Glu Leu Gly Phe Thr Val Phe Ala Gly Val Leu Asn Glu
105 110 115
aat ggc cca gga gct gag gaa ttg cga aga acc tgc tct ccg cgc ctc 498
Asn Gly Pro Gly Ala Glu Glu Leu Arg Arg Thr Cys Ser Pro Arg Leu
120 125 130
tcg gtg ctc caa atg gac atc acg aag cca gtg cag ata aaa gat gct 546
Ser Val Leu Gln Met Asp Ile Thr Lys Pro Val Gln Ile Lys Asp Ala
135 140 145
tac agc aag gtt gca gca atg ctg cag gac aga gga ctg tgg gct gtg 594
Tyr Ser Lys Val Ala Ala Met Leu Gln Asp Arg Gly Leu Trp Ala Val
150 155 160
atc aac aat gct ggg gtg ctt ggc ttt cca act gat ggg gag ctt ctt 642
Ile Asn Asn Ala Gly Val Leu Gly Phe Pro Thr Asp Gly Glu Leu Leu
165 170 175 180
ctt atg act gac tac aaa caa tgc atg gcc gtg aac ttc ttt gga act 690
Leu Met Thr Asp Tyr Lys Gln Cys Met Ala Val Asn Phe Phe Gly Thr
185 190 195
gtg gag gtc aca aag acg ttt ttg cct ctt ctt aga aaa tcc aaa ggg 738
Val Glu Val Thr Lys Thr Phe Leu Pro Leu Leu Arg Lys Ser Lys Gly
200 205 210
agg ctg gtg aat gtc agc agc atg gga gga ggg gcc cca gtg gaa agg 786
Arg Leu Val Asn Val Ser Ser Met Gly Gly Gly Ala Pro Val Glu Arg
215 220 225
ctg gca tct tat ggc tca tca aag gcg gct gtg acc atg ttc tca tca 834
Leu Ala Ser Tyr Gly Ser Ser Lys Ala Ala Val Thr Met Phe Ser Ser
230 235 240
gtt atg aga ctg gag ctt tcc aag tgg gga att aaa gtt gct tcc atc 882
Val Met Arg Leu Glu Leu Ser Lys Trp Gly Ile Lys Val Ala Ser Ile
245 250 255 260
caa cct gga ggc ttc cta aca aat atc gca ggc acc agt gac aag tgg 930
Gln Pro Gly Gly Phe Leu Thr Asn Ile Ala Gly Thr Ser Asp Lys Trp
265 270 275
gaa aag ctg gag aag gac att ctg gac cac ctc ccc gct gag gta cag 978
Glu Lys Leu Glu Lys Asp Ile Leu Asp His Leu Pro Ala Glu Val Gln
280 285 290
gaa gac tac tgc cag gac tac atc tta gca cag cgg aat ttc ctc cta 1026

Glu	Asp	Tyr	Cys	Gln	Asp	Tyr	Ile	Leu	Ala	Gln	Arg	Asn	Phe	Leu	Leu		
	295						300					305					
ttg	atc	aac	tcg	tta	gcc	agc	aag	gac	ttc	tct	ccg	gtg	ctg	cgg	gac	1074	
Leu	Ile	Asn	Ser	Leu	Ala	Ser	Lys	Asp	Phe	Ser	Pro	Val	Leu	Arg	Asp		
	310						315				320						
atc	cag	cat	gct	atc	ttg	gcg	aag	agc	cct	ttt	gcc	tat	tac	acg	cca	1122	
Ile	Gln	His	Ala	Ile	Leu	Ala	Lys	Ser	Pro	Phe	Ala	Tyr	Tyr	Thr	Pro		
	325					330				335					340		
ggg	aaa	ggc	gct	tac	ttg	tgg	atc	tgc	ctt	gct	cac	tat	ttg	cct	att	1170	
Gly	Lys	Gly	Ala	Tyr	Leu	Trp	Ile	Cys	Leu	Ala	His	Tyr	Leu	Pro	Ile		
			345					350						355			
ggc	ata	tat	gat	tac	ttt	gct	aaa	aga	cat	ttt	ggc	caa	gac	aag	ccc	1218	
Gly	Ile	Tyr	Asp	Tyr	Phe	Ala	Lys	Arg	His	Phe	Gly	Gln	Asp	Lys	Pro		
			360					365					370				
atg	ccc	aga	gct	tta	aga	atg	cct	aac	tac	aag	aaa	aag	gcc	ccc		1263	
Met	Pro	Arg	Ala	Leu	Arg	Met	Pro	Asn	Tyr	Lys	Lys	Lys	Ala	Pro			
	375						380				385						
taggcaatgg	aagccctcaa	agaagtcgga	atgtcatagt	cttgaaatga	aagggaaact	1323											
gggaaattgg	gtttctcatt	aaagttgttt	cccactctgt	waaaaaaaaa	aaaaaaaaaa	1383											
aaaaaaaaaga	aaaaaaaaaa	aaaaa				1408											

<210> 112

<211> 387

<212> PRT

<213> Homo sapiens

<400> 112

Met	Ser	Thr	Phe	Phe	Ser	Asp	Thr	Ala	Trp	Ile	Cys	Leu	Ala	Val	Pro		
1			5						10					15			
Thr	Val	Leu	Cys	Gly	Thr	Val	Phe	Cys	Lys	Tyr	Lys	Lys	Ser	Ser	Gly		
		20						25					30				
Gln	Leu	Trp	Ser	Trp	Met	Val	Cys	Leu	Ala	Gly	Leu	Cys	Ala	Val	Cys		
		35					40					45					
Leu	Leu	Ile	Leu	Ser	Pro	Phe	Trp	Gly	Leu	Ile	Leu	Phe	Ser	Val	Ser		
	50					55				60							
Cys	Phe	Leu	Met	Tyr	Thr	Tyr	Leu	Ser	Gly	Gln	Glu	Leu	Leu	Pro	Val		
	65			70						75				80			
Asp	Gln	Lys	Ala	Val	Leu	Val	Thr	Gly	Gly	Asp	Cys	Gly	Leu	Gly	His		
			85					90						95			
Ala	Leu	Cys	Lys	Tyr	Leu	Asp	Glu	Leu	Gly	Phe	Thr	Val	Phe	Ala	Gly		
		100					105						110				
Val	Leu	Asn	Glu	Asn	Gly	Pro	Gly	Ala	Glu	Glu	Leu	Arg	Arg	Thr	Cys		
		115					120					125					
Ser	Pro	Arg	Leu	Ser	Val	Leu	Gln	Met	Asp	Ile	Thr	Lys	Pro	Val	Gln		
	130					135					140						
Ile	Lys	Asp	Ala	Tyr	Ser	Lys	Val	Ala	Ala	Met	Leu	Gln	Asp	Arg	Gly		
	145			150				155						160			
Leu	Trp	Ala	Val	Ile	Asn	Asn	Ala	Gly	Val	Leu	Gly	Phe	Pro	Thr	Asp		
			165					170						175			
Gly	Glu	Leu	Leu	Met	Thr	Asp	Tyr	Lys	Gln	Cys	Met	Ala	Val	Asn			
		180					185					190					
Phe	Phe	Gly	Thr	Val	Glu	Val	Thr	Lys	Thr	Phe	Leu	Pro	Leu	Leu	Arg		
	195						200				205						
Lys	Ser	Lys	Gly	Arg	Leu	Val	Asn	Val	Ser	Ser	Met	Gly	Gly	Gly	Ala		
	210					215					220						
Pro	Val	Glu	Arg	Leu	Ala	Ser	Tyr	Gly	Ser	Ser	Lys	Ala	Ala	Val	Thr		
	225				230				235					240			
Met	Phe	Ser	Ser	Val	Met	Arg	Leu	Glu	Leu	Ser	Lys	Trp	Gly	Ile	Lys		
			245					250						255			
Val	Ala	Ser	Ile	Gln	Pro	Gly	Gly	Phe	Leu	Thr	Asn	Ile	Ala	Gly	Thr		

				260					265				270				
Ser	Asp	Lys	Trp	Glu	Lys	Leu	Glu	Lys	Asp	Ile	Leu	Asp	His	Leu	Pro		
		275						280				285					
Ala	Glu	Val	Gln	Glu	Asp	Tyr	Cys	Gln	Asp	Tyr	Ile	Leu	Ala	Gln	Arg		
		290				295					300						
Asn	Phe	Leu	Leu	Leu	Ile	Asn	Ser	Leu	Ala	Ser	Lys	Asp	Phe	Ser	Pro		
305					310					315					320		
Val	Leu	Arg	Asp	Ile	Gln	His	Ala	Ile	Leu	Ala	Lys	Ser	Pro	Phe	Ala		
			325						330				335				
Tyr	Tyr	Thr	Pro	Gly	Lys	Gly	Ala	Tyr	Leu	Trp	Ile	Cys	Leu	Ala	His		
			340					345				350					
Tyr	Leu	Pro	Ile	Gly	Ile	Tyr	Asp	Tyr	Phe	Ala	Lys	Arg	His	Phe	Gly		
		355					360				365						
Gln	Asp	Lys	Pro	Met	Pro	Arg	Ala	Leu	Arg	Met	Pro	Asn	Tyr	Lys	Lys		
	370					375					380						
Lys	Ala	Pro															
385																	